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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scription	. 6	16699 Seque	293014 Homo sapien AL121601 Human DNA	α.	AX412131 Sequence	AX4295/5 Sequence AR103281 Sequence	AX412118 Sequence	U45880 Human X-lin BC032729 Homo sapi	E31042 Method for	U32974 Human IAP-1 782207 Homb canion	AL390123 Himan DNA	AC111718 Rattus no	AC151311 NOWO Sapi AC069566 HOMO Sapi	AC027582 Homo sapi	AC0094/6 Homo sapi AC023053 Homo sapi	AC093503 Homo sapi	AC025983 Homo sapi AC005230 Homo sapi	AL445903 Human chr	AC026306 Homo sapi	AC120024 HOMO SAPI AC090411 HOMO SAPI	AC000021 Origins o	AC000022 Genomic s AF164343 Homo sani	AC010089 Homo sapi	AF241729 Homo sapi	AC025679 Homo sapi	AC100757 Homo sapi	ACUZ331U HOMO Sapı ACOO6983 Homo sapı	AC006990 Homo sapi	AC006338 Homo sapi	ACUZZZIZ HOMO Sapi) ທ	AP001401 Homo sapi AL451141 Human DNA			linear PAT 14-FEB-2001					Baird, S., Tsang, B.K. and	diagnosis and treatment of
SUMMARIES	AR106397	AR116699	HS16/P19 HSD:1315G1	HS424J12	AX412131	AX4295/5 AR103281	AX412118	HSU45880 BC032729	E31042	HSU32974 HSA24.112	AL390123	AC111718	AC151311 AC069566	AC027582	AC023053	AC093503	AC025983 AC005230	CNS07EEU	AC026306	AC120024 AC090411	HSAC000021	AC000022 AF164343	AC010089	AF241729	AC025679	AC100757	AC023310 AC006983	AC006990	AC006338	AC022212	AC010088	AP001401 AL451141	ALIGNMENTS		5232 bp DNA		927			5232) MacKenzie, A.E., Liston, P.,	tion of IAPS for the
% Query Match]	100.0 5232 6	100.0 5232 6	67 3 133391 9	67.3 201197 2	43.5 3000 6	38.7 2404 6	38.0 2540 6	38.0 2540 9 33.6 2086 9	29.8 1659 6	29.8 1659 9 17 4 201197 2	2.8 158093 9	2.4 185771 2	2.1 69937 2	2.1 150107 2	2.1 313264 2	2.1 147598 9	2.1 173316 2	2.0 145556 9	2.0 160653 2	2.0 40271 2	2.0 40328 9	2.0 43795 9	2.0 103356 9	2.0 141580 9	2.0 166937 9	2.0 171987 9	2.0 17/355 9 2.0 180345 9	2.0 184637 2	2.0 186838 9	2.0 18/313 9	2.0 199458 9	103 2.0 207471 2 102 1.9 63966 9			AR106397	5	AR106397.1 GI:1282092	Unknown.	ified.	es 1 to k,R.G.,	Pratt, C. Detection and modulation
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ATTCATAGTATACTGATTTAATTTCTAAGTGTAAGTGAATTAATCATCTGGATTTTTTAT **AAAGCGTATTTAATGATAGAATACTATCGAGCCAACATGTACTGACATGGAAAGATGTCA AAGATATGTTAAGTGTAAAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGATCA** TGTGGATGAAAAATATTTCTGAGTGGTAGTTTTTTTGACAGGTAGACCATGTCTTATCTTG TTTAAAGTTATAAACACGTACTTGTGCGAATTATTTTTTAAAGTGATTTGCCATTTTTG **AAGTATGTATGTTTTTAATATGCATAGAACAAAAGATTTGGAAAGATATACACCAAACTG** GTATTACTTTTGTAATCAGAATTTTTAGAAAGTATTTTGCTGATTTAAAAGGCTTAGGCAT GTTCAAACGCCTGCAAAACTACTTATCACTCAGCTTTAGTTTTCTAATCCAAGAAGGCA TITCAAAATAAGTATITCIGATITTGTAAAATGAAATATAAAATATGTCTCAGATCTTCC TATCATCTTGTATCTTAAAGTTTCATGTGAGTTTTTACCGTTAGGATGATTAAGATGTAT GAAAGATAGAGATTGTTTTTAGAGGTTGGTTGTTGTGTTTTAGGATTCTGTCCATTTTCT

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941 941 001 001 061	3121 3121 3181 3181 3241	3301 3301 3361 3361	3421 3421 3481 3481	54 54 60	3661 3661 3721 3721	3781 3781 3841 3841	3901 3901 3961 3961
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Qy Dp	4021	AAACTTGTATGTTTAGAGTTAAGCAAGACTTTTTTCTTCCTCTCCATGAGTTGTGAAAT 4080
Qy	4081	TTATTTTAAGAATTGTTTAGAAATGCTGT 414
qq	4081	aatgcacaacgctgatgtggctaacaagtttatttaagaattgttagaaatgct
Oy (14	OI C
a ë	4141	ICAGGITICITABARICACICAGCACICCAACITICIAARITITIGGAGACITA 420
qq	20	26
Qy	4261	GATCATTTGCAAAAGTCAAAAACTATAGCCATÁTCCAAATCTTTTCCCCT
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qq	4321	rcrcagigiciacaigragaciaiicciiiicigiaiaaagiicaciciagg
Qy	4381	CAAGTCACCACTTATTTACATTTTAGTCATGCAAAGATTCAAGTAGTTTTGCAATAAGT 4440 [1] [
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Qy	4501	SOTTITAGGALTTACAAACTAAATTCCAGTTAATTAATTAATAGCTTTATATTGC
qq	4501	AACTGGTTTTAGCATTTACAAACTAAATTCCAGTTAATTAA
οy	4561	TITCCIGCTACATITGGITTITTCCCCTGTCCCTTGATTACGGGCTAAGGTAGGGTAAG 4620
qq	4561	CCTGCTACATTTGGTTTTTTCCCCTGTCCTTTGATTACGGGCTAAGGTAGGGT
Oy	4621	ANNGGGTGTAGTGAGTGTATATATGTGTTTTGGCCCTGTGTATTATGATATTTTGTTAT 4680
Ор	4621	SGGTGTAGTGAGTGTATATATATGTGATTTGGCCCTGTGTATTATGATATTTTGTTA
δŏ	68	74
ф	œ	STTGTTATTATTTACATTTCAGTAGTTGTTTTTTGTGTTTCCATTTTAGGGGAT 474
δλ T	4 .	Ō
QQ	4	ITIGTATITIGAACTAIGAATGGAGACTACCGCCCCAGCATTAGTTICACATGATA 480
ΟŽ	80	98
셤 .	0	CCTTTAAACCCGGAATCATTGTTTTATTTCCTGATTACACAGGTGTTGAATGGGGAAA 486
Qy	4861	GGGGCTAGTATATCAGTAGGATACTATGGGATGTATATATA
QO	4861	GGGCTAGTATATCAGTAGGATATACTATGGGATGTATATATA
ΟŊ	4921	ATGAAATAAAATGGGGCTGGGCTCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGG 4980
qa	4921	SAAATAAAATGGGGCTGGGCTCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGG 4
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qq	4981	<u>TGAGGCAGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAA</u>
QY	5041	10
qq	5041	CCGTCTCTACTAAAAAACAGAAAATTAGCCGGGGGGGGGG
Qy	5101	GCTACTCGGGAGGCTGAGGCAGGAGAATGGTGTGAACCCGGGAGGCAGAGCTTGCAGTGA 5160

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                                                                                                                                                                                                                                                                                     HTG 10-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 122742)
Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Sep 9, 2000 this sequence version replaced gi:6981883.
                                                         5161 GCCGAGATCTCGCCACTGCACTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTCAAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: XGAP4: version 4.5 Sequencing vector: M13; M77815; 18% of reads Sequencing vector: plasmid: L0875; 81% of reads Chemistry: Dye-terminator ABI; 100% of reads Consensus quality: 118637 bases at least Q40 Consensus quality: 120866 bases at least Q30 Consensus quality: 120866 bases at least Q20 Insert size: 121842; sum-of-contigs Quality coverage: 6.65x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                     DNA linear
RP1-167P19 map q25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50765 50864: gap of 100 bp
50865 60908: contig of 10044 bp in length
60909 61008: gap of 100 bp
61009 90700: contig of 28632 bp in length
90701 90800: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26985 27084; gap of 100 bp 27085 36741; contig of 9657 bp in length 36742 36841; gap of 100 bp 100 bp 3842 40799; contig of 3857 bp in length 40799 40898; gap of 100 bp 50764; contig of 9866 hn in length 40899 50764; contig of 9866 hn in length
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18445 24822: contig of 6378 bp in length
24823 24922: gap of 100 bp
24923 26984: contig of 2062 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p of 100 bp
contig of 9866 bp in length
                                                                                                                                                                                                                                                                                 HS167P19 122742 bp DN
Homo sapiens chromosome X clone RP1-1
IN PROGRESS ***, 10 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: humquery@sanger.ac.uk
------ Project Information
Center project name: dJ167P19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                 293014.2 GI:10045109
HTG; HTGS_PHASE1; HTGS_CANCELLED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Sanger Centre
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                                                                                                                                                                5221 AAAAAAAAAG 5232
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                                                                                                                                                                                                                                                                                                                                                                                                              human.
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HS167P19/c
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AUTHORS
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KEYWORDS
SOURCE
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COMMENT

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TTGAATGTGTGATGTGAACTGACTTTAAGTAATCAGGATTGAATTCCATTAGCATTTGCT 88231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1332 AGAGATTAGTACTGAAGAGCAGCTAAGGCGCCTGCAAGAGAGAAAGGTTTGCAAAAATCTG 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1392 TATGGATAGAAATATTGCTATCGTTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACA 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGAATGTGTGATGTGAACTGACTTTAAGTAATCAGGATTGAATTCCATTAGCATTTGCT 1631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 122742;
90801 101526: contig of 10726 bp in length
101527 101626: gap of 100 bp
101627 122742: contig of 21116 bp in length.
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                                         7 122742: contig of 21116 bp in length.
Location/Qualifiers
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Pred. No. 0;
0; Mismatches
                                                                                                   /organism="Homo sapiens"
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99.8%;
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Matches 3893; Conservative
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Db 87030 TGTACACTGCTTGTAGTTATAGT Qy 2892 ATCTTAAAGTTTCATGTGAGTTT ACCTO ATCTTAAAGTTTCATGTGAGTTT ACCTO ATCTTAAAGTTTCATGTGAGTTT	2952 2952 86910	Qy 3012 TGAAATAAATGTTCTCTCAAGAT 	3072	3132	3192 86670	3252	3312		3432	3492	3552			3732 86130		&	Qy 3912 AGTCAGGTAGGTAGTTCATCTA
 ATGTAT 88051 	TTCAGAT 87991 CCCCCAAT 1931 87931		AAGITAT 2051 AAGITAT 87811	CGTATTT 2111 CGTATTT 87751	TATGTTA 2171 TATGTTA 87691	ATGTATG 2231 ATGTATG 87631	ATGIGGT 2291 ATGIGGT 87571	GGCCTTT 2351 GGCCTTT 87511	TACTTT 2411 FACTTT 87451	AAACGCC 2471 AAACGCC 87391	AGTTAAC 2531 AGTTAAC 87331	GATGAAA 2591 			AAAGATC 2771 AAAGATC 87091	GCATGTT 2831 GCATGTT 87031	ATCTIGT 2891
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	88050 ACTGATTTAATTTCTAAGTGTAAC 1872 AGGCTTAACAAATGGAGCTTTCTC 87990 AGCCTTAACAAATGGAGCTTTCTC	1932 CACATAATTTGTTTTGTGAAAA 	1992 ATTGTTTTAGAGGTTGGTTGTTI 	2052 AAACACGTACTTGTGCGAATTAT7 	2112 AATGATAGAATACTATCGAGCCAA 	2172 AGTGTAAAATGCAAGTGGCAAAA(2232 TTTTTAATATGCATAGAACAAAK 	2292 TTCTCTTCGGGAGGGGGGGATTC	2352 TCACTTTCTACTTTTTCATTTTC 	2412 GTAATCAGAATTTTTAGAAAGTA) 	2472 TGCAAAACTACTTATCACTCAGC3 	2532 CTTTTGGTGCCAATGTGAAATGT 	2592 AATATTECTGAGTGGTAGTTTTT 	2652 GTATTTCTGATTTTGTAAAATGAA 	2712 AAGGATTCATCCTTAATCCTTGC3 	2772 TTTGTTAACTCAGTATTTTAAAC7 	2832 TGTACACTGCTTGTAGTTATAGTC
Db 881 Qy 16	Db 88(Qy 16 Db 879	Qy 15 Db 879	Qy 19 Db 878	Oy 20 Db 878	Qy 21 Db 877	Qy 21 Db 876	Qy 23 Db 876	Qy 22 Db 87	Qy 23	Qy 24	Oy 24	Qy 25 Db 873	Oy 25 Db 873	Oy 26	Qy 27 Db 871	Qy 27 Db 870	Qy 28

AGTIGTTAGCCAAGGACTCAAGGACTGAATTGTTTAA 3971 86671 86611 86551 86371 86311 86251 86131 TGACAGCTTTCCATGTTGAGATTCTCATATCATCTTGT 86971 3011 3071 3131 3251 3311 3431 3491 3551 3611 3671 3731 3791 3851 3911 ITCCTTAAAACCTCTTGGAAATTATAAAAATATTGGCAA **NATATITITAAAAAACACTIGAATAAGAATCAGTAGGG** GCCTCATAGAACGTCCAGGGTTTACATTACAAGATTCT **ICTITAAGTGATATTCATTTAAAACATTGCAAATTTATT** GAGATGGAGTCTTGTCACCCAGGCTGGAGTGCAG PARCETCE GCCTTCTGGGTTCAAGCGATTCTCGTGCCTC CAGTICITCACCITTGCACTGICTGCCACTTAGITTGG TTGGTCTGTATAGTCTAGACTTTAAATTTAAAGTTTTC AATTTTTAAAATATGTTTTCCAGGACACTTCACTTCCA CATTIGITITICITGGCTAGTAATAGTAGTAGATACTIC CCCAAAGTGCTGGGATTACAGGCTTGAGCCACCACGCC **AAATGAGAGTTTTAAAATTAAATGACTGCCCTGTT**

- di - di Talana

Qy Db	3972 85890	CATAAGGCTTTTCCTGTTCTGGGAGCCGCACTTCATTAAAATTCTTCTAAAACTTGTATG 4031
Qy Dp	4032	TTTAGAGTTAAGCAAGACTTTTTTTTTTCTCCTCCATGAGTTGTGAAATTTAATGCACAA 4091
Oy Dp	4092	CGCTGATGTGGCTAACAAGTTTATTTTAAGÅATTGTTTAGAAATGCTGTTGCTTCAGGTT 4151
oy ob	4152 CTTAAAAT 85710 CTTAAAAT	CACTCAGCACTCCAACTTCTAAATTTTTGGAGACTTAACAGCATTTGT 4211
0y Dp	4212 CTGTGTTT	GAACTATAAAAAGCACCGGATCTTTCCATCTAATTCCGCAAAAATTGATCA 4271
Qy Dp	4272 85590	TTTGCAAAGTCAAAACTATAGCCATATCCAAATCTTTTCCCCTCCCAAGAGTTCTCAGT 4331
Qy Dp	4332	GTCTACATGTAGACTATTCCTTTTCTGTATAAGTTCACTCTAGGATTTCAAGTCACCAC 4391
0y 0b	4392	TTATTTTACATTTTAGTCATGCAAAGATTCAAGTAGTTTTGCAATAAGTACTTATCTTTA 4451
Qy Dp	4452	TITGTAATAATITAGICIGCIGAICAAAAGCAITGICITAATITITGAGAACIGGITITA 4511
Qy Db	4512 G 1 85350 G	CATTTACAAACTAAATTCCAGTTAATTAATTAATTATATTATATTGCCTTTCCTGCTAC 4571
oy B	4572 85290	ATTEGTTTTTCCCCTGTCCCTTTGATTACGGGCTAAGGTAGGANNGGGTGTAG 4631
Oy Op	4632	TGAGTGTATATAATGTGATTTGGCCCTGTGTATTATGATATTTTGTTATTTTTGTTGTTA 4691
QY Dp	4692	TATTATTTACATTTCAGTAGTTGTTTTTGTGTTTCCATTTTAGGGGATAAATTTGTAT 4751
ç, G	4752 85111	TITGAACTATGAATGGAGACTACCGCCCCAGCATTAGTTTCACATGATATACCTTTAAA 4811
Qy Pp	4812	CCCGAATCATTGTTTTATTTCCTGATTACACAGGTGTTGAATGGGGAAAGGGGCTAGTAT 4871
Oy Dp	4872	atcagtaggatatactatgggatgtatatatatcattgctgttagagaaatgaataaa 4931
oy op	4932 T 84931 T	GGGGCTGGGCTCAGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCAGGT 4991
oy B	4992	GGATCACGAGGTCAGGAGACCATCCTGGCTAACACGGTGAACCCCGTCTCTAC 5051

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Direct Submission

Submitted (12-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk

On Mar 6, 2000 this sequence version replaced gi:6983378.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSDJ315G1
133391 bp DNA linear PRI 23-JUN-2000
Human DNA sequence from clone RP1-315G1 on chromosome Xq34-25.
Contains a PDZ (DHK, GLGF) domain protein pseudogene, the API3 gene
for apoptosis inhibitor 3 (XIAP, HILP), a putative novel gene.
ESTS, STSS, GSSs and a putative CpG island, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             t
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 133391)
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RP1-315G1 is from the library RPCI-1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
                               GGCTGAGGCAGAGAATGGTGTGAACCCGGGAGGCAGAGCTTGCAGTGAGCCGAGATCTC 5171
                                                                                                                                                                                                                                                                           5052 TAAAAAAACAGAAAATTAGCCGGGCGTGGTGGCGGGCGCCTGTAGTCCCAGCTACTCGGGA 5111
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                                                                                                                                                                                                                                           This sequence is the entire insert of clone RP1-315G1 The right end of clone RP6-30A23 is at 100 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; API3; CpG island; DHR; GLGF; HILP; PDZ; XIAP
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AL121601.13 GI:7159760
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VERSION
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AUTHORS
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JOURNAL
                                                        84811
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HSDJ315G1
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us-09-974-592-3.rge

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67.3%; Score 3523; DB 9; Length 133391; 99.8%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                               / 43402. . 4327/3 / 70402- mmatch: STS: Em:L/7/256" | 55942. . 56315 | 700te="match: STS: Em:L/40935" | 700te="match: SFS: Em:L/40935" | 76488. . 56535 | 70468- . 24 copies 2 mer at 77% conserved" | 63199. . 65252 | 700te="27 copies 2 mer tc 87% conserved" | 67078. . 65078 | 700te="match: STS: Em:AL031561" | 700te="match: STS: Em:AL031561" | 700te="match: GSS: Em:A048834 Em:A0540857" | 700te="match: GSS: Em:A048833 | 700te="match: GSS: Em:A04333" | 700te="match: GSS: Em:A0380019" | 700te="match: GSS: Em:A0405293" | 700te="match: GSS: Em:A040529
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83301. .83356
/note="28 copies 2 mer aa 73% conserved"
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### Complement(6961. 6990)

### Complement(6961. 6990)

### Complement(6961. 6971)

### Complement(6961. 7010)

#### Complement(6991. 7010)

#### Complement(69956. 70137)
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                             complement (40058
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Best Local Similarity 99.8
Matches 3893; Conservative
                                                                                                 repeat_region
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YSEBARLKFRONDPYAHLTPRELASARALYYTGIODQVQCFCGGGKLWBEDCDRAWS
EHRRHFPNCFFVLGRYLLNIRESEDAYSSDRMFPNSTALLPRNSAADYBARIT
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KICMDRNIAIVFYPCGHLVTCKQCAEAVDKCPMCYTVITFKQXISTEGLRRLQBEKLC
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// note="27 copies 2 mer aa 72% conserved"

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// note="match: GSS: Em:AQ03308"

// note="match: GSS: Em:AQ03308"

// note="match: GSS: Em:AQ719253"
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Tr:097111"
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Em:A1598959 Em:A1418337 Em:A1277821 Em:HSCZQG052
Em:AA987840"
                                                                                                                                                                                                                                                                                                                 note-"dJ315G1.1 (PDZ (DHR, GLGF) domain protein
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Oy	1332	AGAGATTAGTACTGAAGAGCAGCTAAGGCGCCTGCAAGAGGAGGAAGCTTTGCAAAATCTG 1391	
Op	35108		
Q	1392	TATGGATAGAAATATTGCTATGGTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACA 1451	
Dp	35168		
Oy	1452	ATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACTTTCAAGCAAAA 1511	
Dp	35228		
oy	1512	AATTTTTATGTCTTAATCTAACTCTATAGTAGGCATGTTATGTTGTTGTTGTTGTGT 1571	
Dp	35288		
Oy	1572	TTGAATGTGTGATGTGAACTTTAAGTAATCAGGATTGAATTCCATTAGCATTTGCT 1631	
Dp	35348		
Oy	1632	ACCAAGTAGGAAAAAAATGTACATGGCAGTGTTTTAGTTGGCAATATAATCTTTGAATT 1691	
Op	35408		
oy	1692	TCTTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTTTTACTGTTATTTAATTGAAA 1751	
O	35468		
δγ	1752 35528	CCATAGACTAAGAATAAGAAGCATCATACTATAACTGAACACAATGTGTATTCATAGTAT 1811 	
g Q	1812 35588	ACTGATTTAATTTCTAAGTGTAAGTGAATTAATCATCTGGATTTTTTATTCTTTCAGAT 1871 	
Oy	1872	AGGCTTAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTAATCTCCCCAAT 1931	
Dp	35648		
g ç	1932 35708	CACATAATTTGTTTTGTGTGAAAAAGGAATAAATTGTTCCATGCTGGTGGAAAGATAGG 1991 	
Q	1992	ATTGTITITAGAGGTTGGTTGTGTTTTAGGATTCTGTCCATTTTCTTTAAAGTTAT 2051	
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Dp	35828		
9.	2112	AATGATAGAATACTATCGAGCCAACATGTACTGACATGGAAAGATGTCAAAGATATGTTA 2171	
Pb	35888		
O D	2172 35948	agtgtaaaatgcaagtggcaaaacactatgtatagtctgagccagatcaaagtatgtat	
oy	2232	TTTTAATATGCGTAGAACAAAGGTTTGGAAAGATATACACCAAACTGTTAAATGTGGT 2291	
B	36008		
ογ	2292 36068	TTCTCTTCGGGGAGGGGGGGTTGGGGGGGGGCCCCAGAGGGGTTTTATAGGGGCCTTT 2351 	
Q Q	2352 36128	TCACTTCTACTTTTTCATTTTGTTCTGTTCGAATTTTTATAAGTATGTAT	

36367 36487 36547 36667 36787 36847 36967 37027 37147 37207 37267 36427 36607 36907 37087 3491 2651 2891 3011 3071 3131 3251 3311 3371 3431 3191 2471 GAAAAGAAGAATAGTTGTTTAAATATTTTTTAAAAAACACTTGAATAAGAATCAGTAGGG GTAATCAGAATTTTTAGAAAGTATTTTGCTGATTTAAAGGCTTAGGCATGTTCAAACGCC TGCAAAACTACTTATCACTCAGCTTTAGTTTTTCTAATCCAAGAAGGCAGGGCAGTTAAC CTTTTGGTGCCAATGTGAAATGTAAATGATTTATGTTTTTCCTGCTTTGTGGATGAAA TGTACACTGCTTGTAGTTATAGTGACAGCTTTCCATGTTGAGATTCTCATATCATCTTGT ATCTTAAAGTTTCATGTGAGTTTTTACCGTTAGGATGATTAAGATGTATATAGGACAAAA TGAAATAAATGTTCTCTCAAGATCCTTAAAACCTCTTGGAAATTATAAAAATATTGGCAA GAAAAGAAGAATAGTTTAAAATATTTTTAAAAACACTTGAATAAGAATCAGTAGGG CACAACAAACCCATTGTAGAGGTGAGTAAGGCATGTTACTACAGAGGAAAGTTTGAGAGT AAAACTGTAAAAATTATATTTTTTTTTGTTGTTCTTAAGAGAAAGAGTATTGTTATGTTC TCCTAACTTCTGTTGATTACTACTTTAAGTGATATTCATTTAAAACATTGCAAATTTATT TGGAGTGATCTCTGCTCACTGCAACCTCCGCCTTCTGGGTTCAAGCGATTCTCGTGCCTC AATATTTCTGAGTGGTAGTTTTTTGACAGGTAGACCATGTCTTATCTTGTTTCAAAATAA TTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGGTAAAAGTAGAAGCATGPT TATAAACTAGAAGTTTAAAAATGCCTCATAGAACGTCCAGGGTTTACATTACAAGATTCT 2712 3492 2412 2472 2652 36428 2832 2892 2952 3012 3072 3132 3252 3312 3372 3432 2532 2592 2772 3192 37088 36188 36308 36368 36488 36548 36608 36668 36728 36788 36848 36908 36968 37028 37148 37208 g q q g g qq g g ò g q QQ g g g ò g g à ò ó q g οy ò ò δ Qγ δ ŏ δ δy δ ò ò ò δý

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38348 ATTTGGTTTTTTCCCCTGTCCCTTTGATTACGGCCTAAGGTAGGGT-AGAGTGGGTGTAG
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Sequencing vector: M13; M77815; 74% of reads
Sequencing vector: M13: M77815; 74% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: humquery@sanger.ac.uk
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Homo sapiens chromosome X clone RP
PROGRESS ***, 15 unordered pieces.
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linear HTG 10-JUL-2001 *** SEQUENCING IN
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 201197)
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On Jan 22, 2001 this sequence version replaced gi:10045116
                                                                                                                                                      TITGAACTATGAATGGAGACTACCGCCCCAGCATTAGTTTCACATGATATACCCTTTAAA
                                                                                                                                                                                                                                      CCCGAATCATTGTTTATTTCCTGATTACACAGGTGTTGAATGGGGAAAGGGGCTAGTAT
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TGAGTGTATATAAGTGATTTGGCCCTGTGTATTATGATATTTTGTTATTTTGTTG
                                                                             TATTATTTACATTTCAGTAGTTGTTTTTTGTGTTTCCATTTTAGGGGATAAAATTTGTAT
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Submitted (09-JUL-2001) Sanger Centre, Hinxton,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.
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* NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                   Insert size: 199797; sum-of-contigs
Quality coverage: 6.87x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148018 148017: gap of 100 bp 148018 176237 contig of 28219 bp in length 176237 18336: gap of 100 bp 176337 187128: contig of 10792 bp in length 187129 187228: gap of 100 bp 187229 190824: contig of 3596 bp in length 18729 190859: gap of 135 bp in length 190960 201197: contig of 10238 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of 1004 bp in length 33: contig of 4004 bp in length gap of 100 bp 45: contig of 31212 bp in length gap of 101 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4155 4254: gap of 100 bp
4255 18703: contig of 14449 bp in length
18704 18803: gap of 100 bp
18804 20941: contig of 2138 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 30470 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14756; gap of 100 bp 147513: contig of 23861 bp in length 188017; app of 100 bp 176236: contig of 28219 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oof 100 bp
contig of 13866 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08: gap of 100 bp 52739: contig of 15131 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 bp
f 4094 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4154: contig of 4154 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p of 105 bp contig of 2496 bp in length
Chemistry: Dye-terminator Big Dye; 0% of reads Chemistry: Dye-terminator ABI; 96% of reads Chemistry: Dye-terminersham; 2% of reads Chemistry: Dye-primer-amersham; 2% of reads Chemistry: Dye-primer Big Dye; 0% of reads Consensus quality: 194333 bases at least Q30 Consensus quality: 196512 bases at least Q30 Consensus quality: 198047 bases at least Q30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52840. .56933
/note="assembly_fragment:01287.0"
57034. .88245
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/note="assembly_fragment:00671.0"
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7note=-assembly_fragment:03624

fragment_chain:2"

35008. .37508

/note="assembly_fragment:00340"
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//note="assembly_fragment:02486
fragment_chain:1"
4255. .18703
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88346: gap of 93386: contig of
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/clone="RP3-424J12"
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20942 21041; gap of
21042 34907; conti
34908 35012; gap of
35013 37508; conti
37509 37608; gap of
37609 52739; conti
52740 5839; gap of
52840 56933; gap of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154118 TATGGATAGAAATATTGCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAACA 154059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCAAGTAGGAAAAAAAAGTACATGGCAGTGTTTTAGTTGGCAATATAATCTTTGAATT 153819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 153818 TCTTGATTTTTCAGGGTATTAGCTGTATTAGTCCATTTTTTTACTGTTATTAATTGAAA 153759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 153758 CCATAGACTAAGAATAAGAAGCATCATACTATAACTGAACACAATGTGTATTCATAGTAT 153699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2052 AAACACGTACTTGTGCGAATTATTTTTTAAAGTGATTTGCCATTTTTGAAAGCGTATTT 2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1392 TATGGATAGAAATATTGCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACA 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1452 ATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACTTTCAAGCAAAA 1511
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              88346. .93386

/note="assembly_fragment:01608"

93487. .123956

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124057. .147917

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176337. .187128

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190925. .201197
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'note="assembly_fragment:01294"
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43266 c 43712 g 57504 t
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Pred. No. 0;
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99.8%;
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Matches 3893; Conservative
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AAAGCGTATT 153399 AAGATATT 2171 AAGATATGTTA 2171	2231 2231 15327	TTAAATGTGGT 2291 TTAAATGTGGT 153219	TAGGGGCCTTT 2351 TAGGGCCTTT 153159	GTATTACTTT 2411 	GTTCAAACGCC 2471 	GGGCAGTTAAC 2531 	TGTGGATGAAA 2591 TGTGGATGAAA 152919	TTTCAAAATAA 2651 TTTCAAATAA 152859	AATTAATTAGT 2711 	ACTAAAAGATC 2771	AGAACCATGTT 2831	TATCATCTTGT 2891 TATCATCTTGT 152619	ATAGGACAAAA 2951 ATAGGACAAA 152559	GTAGATACTTC 3011 	AATATTGGCAA 3071 	AATCAGTAGGG 3131 	TACAAGATTCT 3191
AACACGTACTTGTGCGAATTATTTTTAAAGTGATTTGCCATTTTTGAAAGCGTATTT AATGATAGATACTATCGAACTATTTTTTAAAGTGATTTGCCATTTTTGAAAGCGTATTT AATGATAGAATACTATCGAGCCAACATGTACTGACATGGAAAGATGTCAAAGATATGTTA	AGTGTAAAATGCAAGTGGCAAAACACTATGTATAGTCTCAGCCAGATCAAAGTATGTAT	TTTTTAATATGCATAGAACAAAAGATTTGGAAAGATATACACCAAACTGTTAAATGTGGT 	TTCTCTTCGGGGGGGGGGTTGGGGGGGCCCCCAGAGGGGTTTTATAGGGGCCTTT 	TCACTTTCTACTTTTTCATTTTGTTCTGTTCGAATTTTTTATAAGTATGTAT	GTAATCAGAATTTTTAGAAAGTATTTTGCTGATTTAAAGGCTTAGGCATGTTCAAAGGC 	TGCAAAACTACTTATCACTCAGCTTTAGTTTTTCTAATCCAAGAAGGCAGGGCAGTTAAC 	CTTTTTGGTGCCAATGTGAAATGTAAATGATTTTATGTTTTTCCTGCTTTGTGGATGAAA 	aataltictgagiggiagittitigacaggiagaccaigicttalcitgitcaaataa 	GTATTTCTGATTTTGTAAAATGAAATATAAAATATGTCTCAGATCTTCCAATTAATT	AAGGATTCAFCCTTAATCCTTGCTAGTTTAAGCCTGCCTAAGTCACTTTACTAAAAGATC 	TTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGGTAAAAGTAGAAGCATGTT }	TGTACACTGCTTGTAGTTATAGTGACAGCTTTCCATGTTGAGATTCTCATATCATCTTGT 	atcttaaagtttcatgtgagttttaccgttaggatgattaagatgtttatgagacaaa 	TGTTAAGTCTTTCCTCTACCTACATTGTTTTCTTGGCTAGTAATAGTAGTAGTACTTC 	TGAAATAAATGTTCTCTCAAGATCCTTAAAACCTCTTGGAAATTATAAAAATATTGGCAA 	GAAAAGAAGAATAGTTGTTTAAATATTTTTAAAAACACTTGAATAAGAATCAGTAGGG 	TATAAACTAGAAGTTTAAAAATGCCTCATAGAACGTCCAGGGTTTACATTACAAGATTCT
153458 22112 2	2172 53338	2232 153278	2292 : 153218 :	2352	2412 (153098 (2472 153038	2532 (152978 (2592 <i>i</i> 152918 <i>i</i>	2652 (152858 (2712 152798	2772	2832 152678	2892 i	2952 152558	3012	3072 (3132
od of		Qy Dp	Oy Dp	Qy Dp	Qy	Oy Dp	Oy Dp	oy og	Qy Dp	QV Dp	Oy Op	Oy Db	Qy Db	Qy Dp	Qy Db	Qy Db	ογ

152378 TATAAACTAGAAGTTTAAAAATGCTTCATAGAACGTCCAGGGTTTACATTACAAGATTCT 152319 152199 152139 152079 152019 151899 151839 151779 DD 151778 TCTGTTTTAGTATGTAAATCCTCAGTTCTTCACCTTTGCACTGTCTGCCACTTAGCTTTGG 151719 151479 151419 151359 3851 4211 3371 3431 3551 3611 3671 3731 3791 4031 4151 4271 3491 3852 TACAAGGGAGAAAAGTGTTAAAATTTTTAAAATATGTTTTCCAGGACACTTCACTTCCA 3911 151958 TITITAGTAGAGGGGGTITCACCATGTTGGCCAGGCTGGTATCAAACTCCTGACCTCA 151838 CGCCTAAAACATTGCAAATTTAAATGAGAGTTTTAAAATTAAAATAATGACTGCCCTGTT 3792 TTATATAGTCATTAACTTGAATTTGGTCTGTATAGTCTAGACTTTAAAATTTAAAGTTTTC CATAAGGCTTTTCCTGTTCTGGGAGCCGCACTTCATTAAAATTCTTCTAAAACTTGTATG Db 151538 CATAAGGCTTTTCCTGTTCTGGGAGCCGCACTTCATTAAAATTCTTCTAAAACTTGTATG 3372 TTATTTATTTAATTTTCTTTTGAGATGGAGTCTTGCTTGTCACCCAGGCTGGAGTGCAG TTTTTAGTAGAGGGGGTTTCACCATGTTGGCCAGGCTGGTATCAAACTCCTGACCTCA CGGCTAAAAACATTGCAAATTTAAATGAGAGTTTTAAAAATTAAAATAATGACTGCCCTGTT TCTGTTTTAGTATGTAAATCCTCAGTTCTTCACCTTTGCACTGTCTGCCACTTAGTTTGG TTTAGAGTTAAGCAAGACTTTTTTTTTCTTCCTCCATGAGTTGTGAAATTTAATGCACAA CGCTGATGTGCCTAACAAGTTTATTTAAGAATTGTTTAGAAATGCTGTTGCTTCAGGTT CITAAAAATCACTCAGCACTCCAACTTCTAATCAAATTTTTGGAGACTTAACAGCATTTGT 4212 CTGTGTTTGAACTATAAAAAGCACCGGATCTTTTCCATCTAATTCCGCAAAAATTGATCA TCCTAACTTCTGTTGATTACTACTTTAAGTGATATTCATTTAAAACATTGCAAATTTATT 3312 3552 3672 3732 3972 4032 4092 3192 152198 151718 4152 152318 151418 151358 g g g g 셤 δ Op 셤 οp οy g g Db δ g g g δλ ŏ ò ò δλ ŏ ŏ ò δλ δλ ŏ δ δ òγ

Euteleostom1;

Craniata; Vertebrata; E Catarrhini; Hominidae;

Chordata; Primates;

Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria;

human

(CA)

Inc.

; Aegera Therapeutics

Korneluk, R.G., Lacasse, E., Baird, S., Antisense jap nucleic acids and uses Patent: WO 0226968-A 231 04-APR-2002; University of Ottawa (CA); Aegera Th Location/Qualifiers

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Oy Dp	241	GTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCCAAAT 300 	
Qy Dp	301	TGCAGATTTATCAACGGCTTTTATCTTGAAAATAGTGCCACGCAGTCTACAAATTCTGGT 360 	
Qy Db	361	ATCCAGAATGGTCAGTACAAAGTTGAAAACTATCTGGGAAGCAGAGATCATTTTGCCTTA 420 	
Oy Dp	421	GACAGGCCATCTGAGACACATGCAGACTATCTTTGAGAACTGGGCAGGTTGTAGATATA 480 	
Qý Dp	481	TCAGACACCATATACCCGAGGAACCCTGCCATGTATAGTGAAGAAGCTAGATTAAAGTCC 540 	
oy D	541	TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGGTTAGCAAGTGCTGGACTC 600	
OŞ Dp	601	TACTACACAGGTATTGGTGACCAAGTGCATTTGTTGTGGTGGAAAACTGAAAAAT 660 	
Qy Dp	661	TGGGAACCTTGTGATCGTGGTCAG-AACACAGGCGACACTTTCCTAATTGCTTCTT 719 	
O. D.	720	TGTTTTGGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTTCTGATAGGAA 779 	
Oy Dp	780	TTTCCCAAATTCAACAAATCTTCCAAGAAATCCATCCATGGCAGATTATGAAGCACGGAT 839 	
O.y GD	840	CTTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTTGCAAGAGCTGGATT 899 	
Oy Dp	900	TTATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGAGGGGGGGTAACTGA 959 	
Oy Dp	960	TTGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAATA 1019 	
Oy Db	1020	TCTGTTAGAACAGAAGGACAAGAATATAAACAATATTCATTTAACTCATTCACTTGA 1079 	
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Qy Dp	1200	Taagaaataatiggaggaaaaaattcagatatctgggagcaactataaatcacttgaggt 1259 	
Oy Dp	1260	TCTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGAC 1319 	

oy Oy	1320	TTCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTAAGGCGCCTGCAAGAGGAGAAGCT 1379
Oy Dp	1380	TIGCAAAATCTGTATGGATAGAAATATTGCTATCGTTTTTGTTCCTTGTGGACATCTAGT 143
P G	1440	TTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTAC 14
go do	1500	TITCAAGCAAAAAITITIAIGICITAAICIAACTCIAIAGTAGGCAIGITAIGIT
Oy Dp	1560 1561	8 - 8 3 - 8 3 - 8
Qy	1620 1621	FAT 167
Oy Op	1680 1681	AATCTTTGAATTTCTTGATTTTCAGGGTATTAGCTGTATTATCCATTTTTTTT
Qy Dp	1740	STG 179 STG 180
Qy	1800	TTA 185
oy Op	1860 1861	TICTITICAGATAGGCTTAACAAATGGAGCTITCTGTATATAAATGTGGAGATTAGAGTT 1
Oy Op	1920 1921	AATCTCCCCAATCACATAATTGTTTGTGTGAAAAAGGAATAAATTGTTCCATGCTGGT 197
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Qy Db	2280	

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Bennett,C.Frank, Ackermann,E.J. and Cowsert,L.M. Antisense modulation of X-linked inhibitor of apopatent: US 6087173-A 1 11-JUL-2000;
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/map="xq24-25"
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                                                                              ATTCATAGTATACTGATTTAATTTCTAAGTGTAAGTGAATTAATCATCTGGATTTTTAT
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Suppression of apoptosis in mammalian cells by NAIP and
family of IAP genes
Nature 379 (6563), 349-353 (1996)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; I
1 (bases 1 to 2540)
Liston, P., Roy, M., Tamai, K., Lefebvre, C., Baird, S.,
Cherton-Horvat, G., Farahani, R., McLean, M., Ikeda, J., I
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Submitted (16-JAN-1996) Stephen D. Baird,
Eastern Ontario, Genetics, 401 Smyth Rd.,
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Submitted (06-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA.

NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Contact: Mrayed by: National Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@npin.nih.gov/
Contact: nisc_mgc@npin.nih.gov/
Contact: Nik Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W. Bouffard, G.G., Breen, K., Brinkley, C., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P. J., Touchman, J.W.,
Tsurgeon, C., Vogt., J.L., Waller, M.A.,
Young, A., Zhang, L.-H. and Green, E.D.
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YSEEARLKSFQNWPDYAHLTPRELASAGLXYTGIGDQVQCFCCGGKLKNWEPCDRAWS
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YSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAKWYPGCKYLLEGK
GQEYINNIHLTHSLEBECLVATTEKPPSLTRRIDDTIRQNPWYGEAIRAGFSFKDIKKI
MEEKIQISGSNYKSLEVLVATLVARDKDSMQDESSQTSLQKEISTEEQLRRLQEEKLC
KICMDRNIATVFVPGALLYCKQCAEAVDKCPMCYTVITFKQKIFMS"
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/db_xref="Laxon:9606"
/clone="MGC:45369 IMAGE:5532247"
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Best Local Similarity 99.9
Matches 1997; Conservative
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PN JP 1999326328-A/2

PN JP 199326328-A/2

PF 13-WAY-1998 JP 1998130378

PR 13-WAY-1998 JP 1998130378

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PC GOIN33/566 A61K38/00, A61K38/00, A61K38/00, A61K39/395,

PC A61K39/395,

PC A61K45/00, A61K45/00, A61K45/00, C07K7/06, C07K7/08, C07K14/47, PC GOIN33/536,

PC GOIN33/536,

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PC A61K37/02, A61K37/02, A61K37/02, A61K37/02,

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Pred. No. 0;
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TIAAAAAACTITIGCIAATITICCAAGIGGIAGICCIGITICAGCAICAACACIGGCACGA 228
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0; Mismatches
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163. .363
/note="IAP repeat"
574. .774
/note="IAP repeat"
877. .1068
/note="IAP repeat"
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A conserved family of cellular genes related to the baculovirus iap gene and encoding apoptosis inhibitors
BENDO J. 15 (11), 2685-2694 (1996)
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STLARAGFLYTGEGDTWCESCHAAVDRWOYGDSAVCRHRKGVPDRETINGFYLENSA
STLARAGFLYTGEGDTWLGSRDHFALDRPSETHADYLLRTKGVVDISDTIYPRNPAM
YSEBARLKSPONWDVAHLTPRELASAGLYYTGIGDOYOCFCCGGKLKNWEPCDRRWS
EHRRHFPNCFFVLGRNLNIRSESDAVSSDRNFPNSTNLPRNPSMADYEARIFFGTWI
YSVNKEQLARAGFYALGEGDKWCFHGGGGTTDWRPSEDDHAKYPGCKYLLEOK
GOETINNIHTHSLEECLYNTTEKTPSLTRRIDDTIFONPWYGAIRWGFSFKDIKKI
MEEKIQISGSWYKSLEYLYADLVNAQKDSMOPESSQFELØREISTEEDLKRLGEKK
KICMDRNIAIVFVPCGHLVTCKQCAEAVDKCPMCYTVIFFKQKIFMS"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Duckett,C.S. and Thompson,C.B.
Durect Submission
Submitted (01-AUG-1995) Colin Duckett, Howard Hughes Medical
Institute, The University of Chicago, 924 East 57th Street,
Chicago, IL 60657, USA
Location/Qualifiers
              TGCAAAATCTGTATGGATAGAAATATTGCTATCGTTTTTGTTCCTTGTGGACATCTAGTC
                                                                                                                                                                                                   ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACT
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Human IAP-like protein ILP mRNA, complete cds.
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/protein_id="AAC50518.1"
/db_xref="GI:1016688"
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apoptosis; ring finger; zinc finger.
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/organism="Homo sapiens"
/organism="taxon:9606"
/tissue_type="heart"
/clone_lib="lambda gtl0, C
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82. .1575
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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On Jan 22, 2001 this sequence version replaced g1:10045116.
889 TTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTTGCAAGAGCTGGATTT 948
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                                                                                                                                    TGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAATAT
                                                                                                                                                                                                                          1021 CTGTTAGAACAGAAGGGACAAGAATATATAAACAATATTCATTTAACTCATTCACTTGAG
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                                            901 TATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGAGGAGGGCTAACTGAT
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* NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 199797; sum-of-contigs
Quality coverage: 6.87x in Q20 bases; sum-of-contigs
                                                                                                                                                                     Assembly program: MGAP4; version 4.5
Sequencing vector: M13; M77815; 74% of reads
Sequencing vector: plasmid; L08752; 25% of reads
Chemistry: Dye-terminator B19 Dye; 0% of reads
Chemistry: Dye-terminator AB1; 96% of reads
Chemistry: Dye-primer-amersham; 2% of reads
Chemistry: Dye-primer-amersham; 2% of reads
Consensus quality: 194333 bases at least Q40
Consensus quality: 196512 bases at least Q30
Consensus quality: 196512 bases at least Q30
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18804 20941: contig of 2138 bp in length
20942 21041: gap of 100 bp
21042 34907: contig of 13866 bp in length
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52739: contig of 15131 bp in length
52839: gap of 100 bp
56933: contig of 4004 bp in length
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88245: contig of 31212 bp in length
946: gap of 101 bp
93386: contig of 5040 bp in length
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4155 4254: gap of 100 bp
4255 18703: contig of 14449 bp in length
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                              Center project name: dJ424J12
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/db_xref="taxon:9606"
Contact: humquery@sanger.ac.uk
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/clone="RP3-424J12"
/clone_lib="RPCI-3"
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93487. 123956
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124057. 147917
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/note="assembly_fragment:03867
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Direct Submission

Loud Submission

Loud Submission

Loud Submission

CBIO 15A, UK. Email enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

On Oct 21, 2001 this sequence version replaced gi:15020926.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
the following the following the primary accession numbers given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158093 bp DNA linear PRI 21-OCT-2001 sequence from clone RP11-566F5 on chromosome 10, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 158093)
Laird, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the feature table with their source databases: Em:, EMBL; SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43184 FGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGGCGACACTTTCCTAATTGCTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                    GTTTTGGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTTCTGATAGGAAT
                                                                                                                                                                                                                                                                                  GTTTTGGGCCGGGAATCTTAATATTTCGAAGTGAATCTGATGCTGTGAGTCTGATAGGAAT
                                                                                                                                                                                                                                                                                                                                                                                       TTCCCAAATTCAACAAATCTTCCAAGAAATCCATCCATGGCAGATTATGAAGCACGGATC
                                                                                                     TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGGCGACACTTTCCTAATTGCTTCTTT
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Human DNA s
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sequence. The true right end of clone \mathrm{RP11-402N18} is at 2000 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     986 AACAACATGCTAAATGGTATCCAGGGTGCAAATATCTGTTAGAACAGAAGGGACAAGAAT 1045
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Best Local Similarity 99.2%; Pred. No. 3.4e-61;
Matches 246; Conservative 0; Mismatches 2; Indels
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1. 158093
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Action/Gualifiers"
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Copyright (c) 1993 - 2002 Compugen Ltd.
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	_		Description	Human XIAP coding	Human digestive sy	Human cDNA encodin	DNA of APP related	Human apoptosis in	Human X-linked inh	Human cDNA encodin	Human XIAP coding	Human digestive sy
SUMMARIES			ID		AAK89468	ABK93875	AAK99405	AAT70836	AAA64901	ABK93869	AAZ48862	AAK89469
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			re Match Length DB]	5232	8763	3000	2404	2540	2540	2540	1659	469
	æ	Query	Match	100.0	48.0	43.5	38.7	38.0	38.0	37.6	29.8	9.0
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7 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	7 4 3 2 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 88 NV55038 stan NV55038; N-NOV-1998 uman XIAP co nhibitor of coliferative	9835693-A2. 9835693-A2. 9-AUG-1998. 9-FEB-1998; 1-FEB-1997; IYOT-) UNIV
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This sequence encodes the human XIAP protein, which is a inhibitor of apoptosis protein (IAP), and can be used in the method of the invention. The method is for enhancing apoptosis in cells from a mammal with proliferative disease by treatment with a compound that inhibits biological activity of an IAP or NAIP polypeptide. The inhibitory compounds are used to treat proliferative diseases, specially cancers of compounds are used to treat proliferative diseases, specially cancers of vorry, breast, pancreas, lymph nodes, kin, blood, lung, brain, kidney, liver nasopharnyx, thyroid, central nervous system, prostate, colon, rectum, cervix or endometrium, particularly to increase their sensitivity to chemotherapeutic agents. High levels of the IAP or NAIP proteins are detected in many cancers and are associated with poor prognosis, resistance to chemotherapeutic agents and mutations in p53 (it is suggested that wild-type p33 suppresses transcription of the IAP or NAIP genes). Transgenic animals are used for testing the effects of antisense oligonucleotides and for screening for the inhibitors.
                                                                                                        Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP or NAIP polypeptide - also methods for prognosis based on presence of IAP and NAIP, specifically applied to cancers involving p53 mutations
                                                                                                                                                                                                                                                   Claim 13; Fig 1; 147pp; English.
                                                    P-PSDB; AAW69294
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Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other; Similarity

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300 300 360 360 420 480 480 AAAACTTGTGTACCTGCAGACATCAATAAGGAAGAAGTTTGTAGAAGAGTTTAATAGA 120 Gaps 9 1 GAAAAGGTGGACAAGTCCTATTTTCAAGAGAAGATGACTTTTAACAGTTTTGAAGGATCT 60 GAAAAGGTGGACAAGTCCTATTTCAAGAGAAGATGACTTTTAACAGTTTTGAAGGATCT GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCCCAAAT ATCCAGAATGGTCAGTACAAAGTTGAAAACTATCTGGGAAGCAGCAGAGTCATTTGCCTTA TTAAAAAACTTTTGCTAATTTTCCAAGTGGTAGTCCTGTTTCAGCATCAACACTGGCACGA GCAGGGTTTCTTTATACTGGTGAAGGAGATACCGTGCGGTGCTTTAGTTGTCATGCAGCT TGCAGATITATCAACGGCTTTTATCTTGAAAATAGTGCCACGCAGTCTACAAATTCTGGT GACAGGCCATCTGAGACACATGCAGACTATCTTTTGAGAACTGGGCAGGTTGTAGATATA TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCCAAGAGAGTTAGCAAGTGCTGGACTC TCAGACACCATATACCCGAGGAACCCTGCCATGTATAGTGAAGAAGCTAGATTAAAAGTCC ö DB 19; Length 5232; Indels .; 0 100.0%; Score 5232; ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches Matches 5232; Query Match 61 121 181 241 241 301 361 421 121 181 301 361 121 181 181 541 g ŏ qq g ð ò ò q δ g ò a g g 셤 å ò ò ò

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1560 1020 1080 1140 1260 1380 1440 1500 840 780 840 960 960 099 720 720 780 900 900 TAGCATTTGCTACCAAGTAGGAAAAAAATGTACATGGCAGTGTTTTAGTTGGCAATATA AAGAAAATAAFGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAGGTT TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTTTTAGTTGGCAATATA GTTTTGGGCCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGGTTCTGATAGGAAT TTCCCAAATTCAACAAATCTTCCAAGAAATCCATCCATGGCAGATTATGAAGCACGGATC TTTACTTTTGGGACATGGATATACTCAGTTAACAAGGACAGCTTGCAAGAGCTGGATTT TGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAATAT CTGTTAGAACAGAAGGGACAAGAATATATAAACAATATTCATTTAACTCATTCACTTGAG AAGAAAATAATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAGGTT CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT TGCAAAATCTGTATGGATAGAAATATTGCTATCGTTTTTGTTCCTTGTGGACATCTAGTC 1441 ACTTGTAAACAATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACT TATTACCCTGATTGAATGTGTGATGTGAACTGACTTTAAGTAATCAGGATTGAATTCCAT TACTACACAGGTATTGGTGACCAAGTGCAGTGCTTTTGTTGTGGTGGAAAACTGAAAAAT TACTACACGGTATTGGTGACCAAGTGCAGTGCTTTTGTTGTGGGGAAAACTGAAAAAT TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGGCGACACTTTCCTAATTGCTTCTTT TTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTTGCAAGAGCTGGATTT TATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGAGGAGGGCTAACTGAT TCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTAAAGGCGCCTGCAAGAGGAGAGGTT TTCAAGCAAAAATTTTTATGTCTTAATCTAACTCTATAGTAGGCATGTTATGTTGTTCT 1021 1021 1081 1081 1201 1201 1261 1321 1321 1381 1381 1441 1501 1501 1561 1621 1621 1681 601 601 661 199 721 721 781 781 841 841 901 901 961 961 1261 1561 g ð δ 염 ò g à qq ð g ò g ŏ q ŏ g δ g δ g ò a g ò g ò Q ŏ q ò g ò ò ò

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			QY	4981 CTGA
δo i	3901	CTTCACTTCCAAGTCAGGTAGGTAGTTCAATCTAGTTGTTAGCCAAGGACTCAAGGACTG 39	qq	 4981 CTGA
9 6	3901	CITCACITICCAAGICAGGIAGGIAGGITCAATCTAGTIGTTAGCCAAGGACTCAAGGACTG	Qy	5041 CCCG
Š 2	3961	AATTGTTTTACATAAGGCTTTTCCTGTGTCTGGGAGCCGCACTTCAAATTCTTCTA	qa	5041 CCCG
3 8	1 100	TO THE TRANSPORT OF THE PROPERTY OF THE PROPER	QY	5101 GCTA
5 6	4021	AAACTISTATATTIAAASTTAASCAAGACTTITTITCTTCCTCCTCCATGAGAT 4080 	qa	5101 GCTA
3 8	1704	MANCI LOTATION LITTOPONO L	Oy	5161 GCCG
ž d	4081	TTANISCACARCICATORIGICGCTAACAAGTTTTTTAAGAATTGTTTAGAATTGCTGT 4140 	qa	5161 GCCG
è	4141	では、	Qy	5221 AAAA
g q	4141	TGCTTCAGGTTCTTAAAATCACTCGGCACTCCAACTTCTAATCAAATTTTTGGAGACTTA	qa	5221 AAAA
οy	4201		RESU	RESULT 2
qq	4201	ACAGCATTIGICIGITIGAACTATAAAAGCACCGGATCTTITCCATCTAATTCCGCA 4260	AAK ID	19468 AAK89468
οy	4261	AAAAITGGATCATTTGCAAAGTCAAAACTATAGCCATATCCAAATCTTTTCCCCCTCCCAA 4320	AC H	AAK89468;
QQ	4261		X E X	05-NOV-20
ογ	4321	GAGTICTCAGTGTCACATGTAGACTATTCCTTTTCTGTATAAAGTTCACTCTAGGATTT 4380	SES	Human dig
qq	4321		X XX	Human; die
οy	4381		K K	ulcerative
qq	4381	CAAGTCACCACTTATTTTACATTTTAGTCATGCAAAGATTCAAGTAGTTTTGCAATAAGT 4440	yy SO	Homo sapie
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ογ	4501	AACTGGTTTTAGCATTTACAAACTAAATTCCAGTTAATTAA	PF	17-JAN-20
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οy	4561		ሟ	24 - FEB - 20
qq	4561	TITCCTGCTACATITGGTTTTTTCCCCTGTCCCTTGATTACGGCTAAGGTAGGGTAAG 4620	PR PR	02-MAR-20 16-MAR-20
Qy	4621		PR PR	17-MAR-20 18-APR-20
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qq	4681		PR PR	07-JUL-20 07-JUL-20
οy	4741		PR PR	11-JUL-20 11-JUL-20
qq	4741		PR PR	14-JUL-20 26-JUL-20
Qy	4801	TACCCTTTAAACCCCGAATCATTGTTTTATTTCCTGATTACACAGGTGTTGAATGGGGAAA	PR PR	26-JUL-20 14-AUG-20
QQ	4801		PR PR	14-AUG-20 14-AUG-20
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O.	4921	ATGAAATAAAATGGGGGTGGGGTCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGG	ጟ <u>ዋ</u> ዋ	14-AUG-20 14-AUG-20 14-AUG-20
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igestive system antigen; gene therapy; cancer; appendicitis; ve colitis; infection; Hirschsprung's disease; chronic colitis; e system disorder; Meckel's diverticulum; ds.
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20000S-0220964.
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24-FEB-2000;

22-MAR-2000;

16-MAR-2000;

17-MAR-2000;

18-APR-2000;

19-APR-2000;

19-APR-2000;

10-JUL-2000;

20-JUL-2000;

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PR 22-ARG-2000; 2000US-0226681.
PR 22-ARG-2000; 2000US-0226681.
PR 22-ARG-2000; 2000US-0226681.
PR 22-ARG-2000; 2000US-0226681.
PR 23-ARG-2000; 2000US-0226681.
PR 20-ARG-2000; 2000US-0227182.
PR 01-SEP-2000; 2000US-022934.
PR 01-SEP-2000; 2000US-023934.
PR 01-SEP-2000; 2000US-02344.
PR 01-SEP-2000; 2000US-02344.
PR 01-SEP-2000; 2000US-023498.
PR 01-SEP-2000; 2000US-02344.
PR 01-SEP-2000;
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CAAACGCCTGCAAAACTACTTATCACTCAGCTTTAGTTTTTCTAATCCAAGAAGGCAGGG 2523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2344 GGGCCTTTTCACTTTTCTACTTTTTCATTTTGTTCTGTTCGAATTTTTTATAAGTATGTA 2403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides the protein and coding sequences of a number of human digestive system antiques. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, becterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or encoding a digestive system antigen of the invention.
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99.8%; Pred. No. 0;
tive 0; Mismatches
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20000S-0249265.
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2000US-0249216.
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2000US-0251869.
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Best Local Similarity 99.8
Matches 2881; Conservative
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18-NOV-2000;
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	GTAGTTTTTGACAGGTAG; 	GTAAAATGAAATATAAAAT! 	AATCCTTGCTAGTTTAAGCC 	ATTTTAAACATCTGTCAGC: 	AGTTATAGTGACAGCTTTC 	TGTGAGTTTTTACCGTTAG(TGTGAGTTTTTACCGTTAG(TCTACCTACATTTGTTTTC: 	TCTCAAGATCCTTAAAACC: CTCAAGATCCTTAAAACC:	TTGTTTAAATATTTTTAAA 	TTAAAAATGCCTCATAGAA(TTAAAAATGCTTCATAGAA	TGTAGAGGTGAGTAAGGCA: 	TTATATTTTGTTGTACTT: 	GATTACTACTTTAAGTGAT/ 	TTCTTTTGAGATGGAGTC: 	CTCACTGCAACCTCCGCCT' 	CTGGAATTACAGGCAGGTG(GGGTTTCACCATGTTGGC 	CTTGCCCTCCCAAAGTGCTC
	GGATGAAAAATATTCTGAGTGGTAGTTTTTGACAGGTAGACCATGTCTTATCTTGTT 	CAAAATAAGTATTTCTGATTTGTAAAATGAAATATAAAATATGTCTCAGATCTTCCAAT 	TAATTAGTAAGGATTCATCCTTAATCCTTGCTAGTTTAAGCCTGCCT	AAAAGATCTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGGTAAAAGTAGA 	AGCATGTTTGTACACTGCTTGTAGTTATAGTGACAGCTTTCCATGTTGAGAGATTCTCATAT 	CATCTTGTATCTTAAAGTTTCATGTGAGTTTTACCGTTAGGATGATTAAGATGTATATA 	GGACAAAATGTTAAGTCTTTCCTCTACCTACATTTGTTTCTTGGCTAGTAATAGTAGTA 	GATACTTCTGAAATAAATGTTCTCTCAAGATCCTTAAAACCTCTTGGAAATTATAAAAAT 	ATTGGCAAGAAAAGAAGAATAGTTTAAAATATTTTTAAAAACACTTGAATAAGAAT 	CAGTAGGGTATAAACTAGAAGTTTAAAAATGCCTCATAGAACGTCCAGGGTTTACATTAC 	AAGATTCTCACAACAAACCCATTGTAGAGGTGAGTAAGGCATGTTACTACAGAGAAAGT 	TTGAGAGTAAAACTGTAAAAATTATATTTTGTTGTACTTTCTAAGAGAAAGAGTATT(TTATGTTCTCCTAACTTCTGTTGATTACTACTTTAAGTGATATTCATTTAAAACATTGCA 	AATTTATTTTATTTATTTAATTTCTTTTGAGATGGAGTCTTGCTTG	GAGTGCAGTGGAGTGATCTCTGCTCACTGCAACCTCCGCCTTCTGGGTTCAAGCGATTCT 	CGTGCCTCAGCTTCCTGAGTAGCTGGAATTACAGGCAGGTGCCACCATGCCCGACTAATT	TTTTTTTTATTTTTAGTAGAGGGGTTTCACCATGTTGGCCAGGCTGGTATCAAACTCC 	TGACCTCAAGAGATCCACTCGCCTTGCCCTCCCAAAGTCCTGGGATTACAGGCTTGAGCC
181 CAC	2584 GGJ 11 241 GGJ	2644 CAJ 11 301 CAJ		2764 AAJ 	2824 AGC 11 481 AGC	2884 CAT	2944 GGJ 	3004 GAY 661 GAY	3064 AT		3184 AAK 841 AAK	3244 TTC 901 TTC	3304 TT 961 TT	3364 AAC 11 1021 AAC	3424 GA(1081 GA(3484 CG	3544 TT 	3604 TG
qq	oy O	oy Og	Qy Dp	Qy Dp	Oy Dp	Oy Dp	Oy Op	O _Y	Q Q	Q q	QY	QY Dp	Qy	ΟΥ Db	oy Op	Qy	Qy Db	Qy

1620 3783 3843 3903 3963 4023 4083 4143 4203 1860 4263 1920 4323 4383 2040 4443 2100 4503 2160 4563 2220 4623 2279 4683 TAACATAAGGCTTTTCCTGTTCTGGGAGCCGCACTTCATTAAAATTCTTCTAAAA 1680 TCAAGAGATCCACTCGCCTTGCCCTCCCAAAGTGCTGGGATTACAGGCTTGAGCC 1320 **IGGTTATATAGTCATTAACTTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTA** TTATTTGTAATAATTTGTCTGCTGATCAAAGCATTGTCTTAATTTTGAGAAC <u> ATGTTTAGAGTTAAGCAAGACTTTTTTTTTTCTTCCTCCATGAGTTGTGAAATTTA</u> GTTCTTAAAATCACTCAGCACTCCAACTTCTAATCAAATTTTTGGAGACTTAACA TGTCTGTGTTTGAACTATAAAAAGCACCGGATCTTTTCCATCTAATTCCGCAAAA TCATTTGCAAAGTCAAAACTATAGCCATATCCAAAATCTTTCCCCCTCCCAAGAG AGTGTCTACATGTAGACTATTCCTTTTCTGTATAAAGTTCACTCTAGGATTTCAA **TACATTTGGTTTTTTCCCCTGTCCCTTTGATTACGGGCTAAGGTAGGGTAAGANN** GTTTCTGTTTTAGTATGTAAATCCTCAGTTCTTCACCTTTGCACTGTCTGCCACT CCAAGTCAGGTAGGTAGTTCAATCTAGTTGTTAGCCAAGGACTCAAGGACTGAAT CAACGCTGATGTGGCTAACAAGTTTATTAAGAATTGTTTAGAAATGCTGTTGC TTAGCATTTACAAACTAAATTCCAGTTAATTAATTAATAGCTTTATATTGCCTTT

us-09-974-592-3.rng

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Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP; Cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer; embryonic development; viral pathogenesis; autoimmune disorder; neurodegenerative disease; multiple sclerosis; lupus erythematosus; herpes virus infection; pox virus infection; adenovirus infection; proliferative disease.
                                                                                                                                                                                                                                                          2759
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             2400 ATTTGTATTTTGAACTATGAATGGAGACTACCGCCCCAGCATTAGTTTCACATGATATAC 2459
                                                                                                      2640 AGGCAGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCC 2699
                                                                                                                                                                                                                                                                                             ATTTGTATTTTGAACTATGAATGGAGACTACCGCCCCAGCATTAGTTTCACATGATATAC 4803
                                                                                          AAATAAAATGGGGCTGGGCTCAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTG 4983
                                                                                                                                                                                                                                                                                                                             GAGATCTCGCCACTGCACTCCAGCCTGGGCAACAGAGCAAGACTCTGTCTAAAAAAA 5223
                                                                                                                                                                                                                                               GTCTCTACTAAAAAACAGAAAATTAGCCGGGCGTGGTGGTGGCGGGCCTGTAGTCCCAGCT
                                             CCTTTAAAACCCGAATCATTGTTTTATTTCCTGATTACACAGGTGTTGAATGGGGAAAGGG
                                                                                                                                                                                     AGGCAGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA encoding inhibitor of apoptosis, XIAP #2.
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of
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                                                                        The Invention relates to an inhibitor of apoptosis (IAP) antisense nucleic acid (I) that inhibits IAP biological activity, regardless of length of the antisense nucleic acid, the IAP proteins may be mouse or human XIAP, HIAPI Or HIAP2. Also included are a pharmaceutical composition comprising a mammalian IAP antisense molecule and a method cenhancing apoptosis in a cell, comprising administering a negative regulator of the IAP anti-apoptotic pathway to the cell. The IAP antisense inhibitor is useful for enhancing apoptosis in a cell in a mammal diagnosed with a proliferative disease. The method is useful for treating a patient diagnosed with a proliferative disease like cancer. The IAP antisense molecule is useful to treat, ameliorate, improve,
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   other
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   treating cancer
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                                                135pp;
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   ď
enhancing apoptosis in
proliferative diseases
                                              Fig 15;
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Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta; amyloid precursor protein; tissue-specific expression control; human APP; APP pathway modulator; gene therapy; gene; ds.
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               ATTCATAGTATACTGATTTAATTTCTAAGTGTAAGTGAATTAATCATCTGGATTTTTAT
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/note= "No start codon"
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TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTGCTGGACTC

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The invention relates to a transgenic fly whose genome comprises DNA percording a polypeptide having the Abeta portion of human amyloid preductor protein (APP), fused to a signal sequence. The DNA sequence encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in the specification. The DNA sequence is operably linked to a tissue-specific expression control sequence. Expression of the sequence gives the fly an altered phenotype. The purpose of the invention is for identifying agents that inhibit or promote the expression and/or function of genes or encoded polypeptides which modify the APP pathway. The agent is a compound, triple helix DNA, antisense oligonuciectide, double stranded RNA molecule, ribozyme, or particularly an antibody. It is used to treat conditions such as Alzheimer's disease. The agent can be used as an APP pathway modulator or in gene therapy. This polynuclectide sequence represents the DNA of the APP related human homologue hCP35211.
                                                                                                                                                               New transgenic fly, containing DNA encoding an Abeta portion of hu
APP, useful for identifying agents which modulate the APP pathway
which can be used to treat Alzheimer's disease -
                                           Ë
                                           Konsolaki
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                                           Freuler
  MBH
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                                         Finelli AL,
  NOVARTIS-ERFINDUNGEN VERW
                                                               Zusman
                                       Dengler UJ,
MWHM, Zusma
                                                                                                    2002-315796/35
                                                                                                    WPI; 2002-315796,
P-PSDB; AAO20511
                                                          Reinhardt
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Gaps ; 2404; DB 24; Length Indels Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 other; ï Score 2027; DE Pred. No. 0; Mismatches 38.78; 99.98; Matches 2317; Conservative Similarity Match Local

5 120 120 180 180 240 300 300 360 360 420 420 480 480 009 9 9 ATCCAGAATGGTCACTACAAAGTTGAAAACTATCTGGGAAGCAGAGATCATTTTGCCTTA GAAAAGGTGGACAAGTCCTATTTTCAAGAGAAGATGACTTTTAACAGTTTTGAAGGATCT AAAACTTGTGTACCTGCAGACATCAATAAGGAAGAAGAATTTGTAGAAGAGTTTAATAGA TTAAAAACTTTTGCTAATTTTCCAAGTGGTAGTCCTGTTTCAGCATCAACACTGGCACA GCAGGGTTTCTTTATACTGGTGAAGGAGATACCGTGCGGTGCTTTAGTTGTCATGCAGCT GTAGATAGATGCCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCCAAAT GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCCAAAT TGCAGATTTATCAACGGCTTTTATCTTGAAAATAGTGCCACGCAGTCTACAAATTCTGGT ATCCAGAATGGTCAGTACAAAGTTGAAAACTATCTGGGAAGCAGAGATCATTTTGCCTTA GACAGGCCATCTGAGACACATGCAGACTATCTTTGAGAACTGGGCAGGTTGTAGATATA TCAGACACCATATACCCGAGGAACCCTGCCATGTATAGTGAAGAAGCTAGATTAAAGTCC TCAGACACCATATACCCGAGGAACCCTGCCATGTATAGTGAAGAAGCTAGATTAAAGTCC TTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTGCTGGACTC 181 361 421 181 121 121 181 241 301 301 361 421 481 g ò 8 ò g 2 8 ò g ò g ò 윤 à 셤 ö 용 ð

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Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of susceptibility to apoptotic disease
                                                                                                                                                                                                                                                                                                  history of genes (AAPT/0816-11) respectively code for a new class of mammalian proteins (AAPT/0816-14) respectively code for a new class of mammalian proteins (AAPT/0816-186) that are inhibitors of apoptosis (IAP). The xiap gene (for X-linked IAP gene) was isolated from a human foetal brain zapil cona library using an X-linked sequence tag site that shows strong homology with the conserved ring zinc finger domain of baculovirus CIAPA and oplay genes. The gene was assigned to chromosome XQ25 by FISH. IAP nucleic acids can be used to express IAP polypeptides in cells and animals to inhibit apoptosis, and as primers and probes to identify and isolate additional IAP genes, as well as in methods for treating diseases and disorders involving apoptosis (anti-apoptotic gene therapy).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAAACTTGTGTACCTGCAGACATCAATAAGGAAGAAGAATTTGTAGAAGAGTTTAATAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 1 other;
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              95US-0576956.
95US-0511485.
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Matches 2040; Conservative
                                                                                               Korneluk RG,
                                                               (UYOT-) UNIV OTTAWA.
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The present invention relates to antisense oligonucleotides designed to Inhibit expression of the human x-linked inhibitor of apoptosis. The present sequence is the x-linked inhibitor of apoptosis. The Modified phosphorothicate 2'-methoxyethyl (2'-MoE) oligonucleotides are more effective inhibitors than unmodified oligonucleotides. The oligonucleotides may be used to inhibit x-linked inhibitor of apoptosis expression in cells and tissues in vitro. The oligonucleotides are also useful for treating animals or humans, prone to a disease associated with X-linked inhibitor of apoptosis. The oligonucleotides may also be used prophylactically to prevent infection, inflammation or tumour formation

G; 773 T; 0 other; BP; 781 A; 415 C; 571 2540 Sednence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an inhibitor of apoptosis (IAP) antisense nucleic acid (I) that inhibitor IAP biological activity, regardless of length of the antisense nucleic acid, the IAP proteins may be mouse or human XIAP, HIAPI. Also included are a pharmaceutical composition comprising a mammalian IAP antisense molecule and a method of enhancing apoptosis in a cell, comprising administering a negative regulator of the IAP anti-apoptotic pathway to the cell. The IAP antisense inhibitor is useful for enhancing apoptosis in a cell in a mammal diagnosed with a proliferative disease. The method is useful for treating a patient diagnosed with a proliferative disease like cancer. The IAP antisense molecule is useful to treat, ameliorate, improve, sustain or prevent proliferative diseases (e.g. ovarian cancer, adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or conditions where apoptosis is involved or implicated (e.g. embryonic devoelopment, viral pathogenessis, autoimmune disorders, neurodegenerative diseases, multiple sclerosis, lupus erythematosus and infection by herpes of the IAP antisense and also in the present sequence is a human IAP
                                                                                                                                                                                                                                                                                                                 ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
              cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP; pancreatic cancer; embryonic development; viral pathogenesis; autoimmune disorder; neurodegenerative disease; multiple sclerosis; lupus erythematosus; herpes virus infection; pox virus infection; adenovirus infection; proliferative disease.
ATCTCCCCAATCACATAATTTGTTTTTGTGAAAAAGGAATAAATTGTTCCATGCTGGTG
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                                                                                                                                                                                                                                                                                      Human cDNA encoding inhibitor of apoptosis, XIAP #1.
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Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta; transforming growth factor-beta activated kinase 1; monocyte migration; TRK1 binding protein 1; extracellular matrix protein production; cell growth inhibitor; beta-amyloid protein deposition; immunosuppression; Transforming growth factor-beta; ds.

sedneuce (first entry)

coding

Human XIAP

24-MAR-2000

AAZ48862

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1281
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                                              ACTGAAGAGCAGCTAAGGCGCCTGCAAGAGGAGAAGCTTTGCAAAATCTGTATGGATAGA 1401
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                                                                                                                                                                                                                                                              GCAGTIGACAAGTGTCCCATGTGCTACACAGTCATTACTTTCAAGCAAAAATTTTTATG 1521
                                                                                                                                                                                                                                                                                                                                                         GATGTGAACTGACTTTAAGTAATCAGGATTGAATTCCATTAGCATTTGCTACCAAGTAGG 1641
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                                   GAGAAAACACCATCACTAACTAGAAGAATTGATGATACCATCTTCCAAAATCCTATGGTA
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This sequence encodes the human XIAP protein.

The invention relates to a method for screening a substance inhibiting the formation of a complex between XIAP and TABL, in which X-linked inhibitor of apoptosis protein (XIAP), transforming growth factor-beta activated kinase 1(TAKI) binding protein 1(TABL) and a substance to be tested are contacted with each other and then the presence or formation of a complex between XIAP and TABL is detected. The substance can be used as a drug for extracellular matrix protein production enhancement, cell growth inhibition, monocyte migration, physiologically active substance induction, immunosuppression, and beta-amyloid protein deposition. A substance inhibiting the formation of a complex between TABL and XIAP as well as between XIAP and TGF-beta (Transforming growth factor-beta) type I and/or type II receptor is useful as a drug.

Screening a substance which inhibits combination of the x-linked inhibitor of apoptosis protein

98JP-0130378 98JP-0130378

13-MAY-1998; 13-MAY-1998;

JP11326328-A.

26-NOV-1999

sapiens

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(MATS/) MATSUMOTO

WPI; 2000-078337/07.

P-PSDB; AAY59451

Japanese

Disclosure; Page 28-30; 43pp;

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                                                                                                                                                                                                           29.8%; Score 1560; DB 21; Length 1659; 99.9%; Pred. No. 0; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                    Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;
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Matches 1610;
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AAZ48862 standard; cDNA; 1659

RESULT 8
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ACAAATTC	71188	CATTTGCC	GTAGA	TTAAA	GCTGG	CTGAP 	TGCTT	ftctgataggaat 	FGAAGCACGGATC 	GCTGG	SCTAACTC	TGCAP TGCAP	TCACT	GATGATA GATGATA	AAGGP	ACTTGAGG	AAGTC?	GAGAA GAGAA	GGACATCT
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man; digestive system antigen; gene therapy; cancer; appendicitis; cerative colitis; infection; Hirschsprung's disease; chronic colitis; gestive system disorder; Meckel's diverticulum; ds.
29 TGCAAAATCTGTATGGATAGAAATATTGCTATCGTTTTTGTTCCTTGTGGACATCTAGTC 1488
                                                                                                                                         01 TICAAGCAAAAATITITATGICITAATCIAACICIATAGIAGGCAIGITATGITGITCI 1560
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TCAGGGTATTAGCTGTATTATCCATTTTTTTACTGTTATTTAATTGAAACCATAGACTA 1761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides the protein and coding sequences of a number of human digestive system antigens. These can be used in the diagnosis, treatment and prevention of digestive system disorders, including cancer, Meckel's diverticulum, bacterial or parasitic infections, appendicitis, Hirschsprung's disease, chronic colitis or ulcerative colitis. The present sequence is a genomic DNA fragment encoding a digestive system antigen of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotides encoding digestive system antigens, useful for diagnosing, treating, preventing and/or prognozing disorders of the digestive system, particularly cancer and cancer metastases -
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100.0%; Pred. No. 1.4e-162;
7ative 0; Mismatches 0;
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2000US-0249299.
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2000US-0250391.
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05-JAN-2001; 2001US-0259678
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AGAATAAGAAGCATCATACTATAACTGAACACAATGTGTATTCATAGTATACTGATTTAA 1821

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conclete acid probes for measuring gene expression in a sample derived from human breast and BT 474 cells. The method involves contacting the probes with a collection of detectably labelled nucleic acids derived from mRNA of human breast, and then measuring the label bound to each probe of the microarray. The probes are useful for verifying the expression of regions of genomic DNA predicted to encode proteins. They are useful for assessing breast disease. Gene expression analysis is useful for assessing the toxicity of chemical expression analysis is useful for assessing the toxicity of chemical expression analysis is useful for assessing the toxicity of chemical expression analysis is useful for assessing the toxicity of chemical diversity of probes for measuring gene expression, with far less bias than expressed sequence tag microarrays. The method is suitable for rapid production of functional information from genomic sequence. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                              1941
                                                    241 AGAATAAGAAGCATCATACTATAACTGAACACAATGTGTATTCATAGTATACTGATTTAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a spatially-addressable set of single exon
                                  1822 TITCTAAGTGTAAGTGAATTAATCATCTGGATTTTTTTATTCTTTTCAGATAGGCTTAACA
                                                                                                            1882 AATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTAATCTCCCCAATCACATATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New spatially-addressable set of single exon nucleic acid probes, useful for measuring gene expression in sample derived from human breast, comprises number of single exon nucleic acid probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; microarray; single exon probe; gene expression; breast;
                                                                                                                                                                                   1942 GITITGIGIGAAAAAGGAAIAAAITGITCCAIGCIGGAAAGAIAGA 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 2279; 327pp + sequence listing; English.
                                                                                                                                                                                                        421 GTTTTGTGTGAAAAAGGAATAAATTGTTCCATGCTGGTGGAAAGATAGA 469
                                                                                                                                                                                                                                                                                                                                                                                                                            Human breast cell single exon nucleic acid probe #2279
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2000US-0207456.
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
04-OCT-2000;
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                                                                                               1332 AGAGATTAGTACTGAAGAGCAGCTAAGGCGCCTGCAAGAGAGAAGCTTTGCAAAATCTG 1391
                                                                                                                                              1392 TATGGATAGAAATATTGCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACA 1451
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                                                                                                            346 ATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACTTTCAAGCAAAA 287
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                                               Length 489;
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                        Sequence 489 BP; 175 A; 90 C; 73 G; 151 T; 0 other;
                                                          Pred. No. 1.7e-161;
                                               DB 22;
                                                      100.0%; Preu. ....
                                             8.9%; Score 466;
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2000US-0207456.
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2000US-02366.
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27-SEP-2000;
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03-AUG-2000;
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                                                                                The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human Hele cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                            ATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACTTTCAAGCAAAA
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                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells –
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100.0%; Pred. No. 1.7e-161;
1ve 0; Mismatches 0; Indels
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                                                              Claim 25; SEQ ID No 2268; 487pp; English
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The present invention relates to novel single exon nucleic acid probes. The present sequence is one such probe. The probes are useful for measuring human gene expression in a human breast sample, where the probe hybridises at high stringency to a nucleic acid expressed in the human breast. The probes are useful for predicting, diagnosing, grading, particular, monitoring and prognosing diseases of the human breast, particularly those diseases with polygenic actiology. The diseases include: breast cancer, disorders of development, inflammatory diseases non-carcinoma tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1512 AATTTTTATGTCTTAATCTAACTCTATAGTAGGCATGTTATGTTGTTCTTATTACCCTGA 1571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 406 TATGGATAGAAATATTGCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGAATGTGTGATGTGAACTGACTTTAAGTAATCAGGATTGAATTCCATTAGCATTTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.7e-161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel single exon nucleic acid probe used in a human breast -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; SEQ ID No 2240; 322pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.9%; Score 466;
                                                                                                                                                                                                                                                                                                                                                                 Rank
                                                                                                                                                                                                                                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                 04-FEB-2000, 2000US-0180312.
26-MAY-2000, 2000US-0207456.
30-UNA-2000; 2000US-0604408.
03-AUG-2000, 2000US-053266.
21-SEP-2000; 2000US-0234687.
27-SEP-2000; 2000US-0234687.
04-OCT-2000; 2000GB-00242633.
                                                                                                                                                                                                                                                                                                                                                                 Chen W,
                                                29-JAN-2001; 2001WO-US00661
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                                                                                                                                                                                                                                                                                                                                                                 Hanzel DK,
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09-AUG-2001
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61 TTGTAATCAGAATTTTTAGAAAGTATTTTGCTGATTTAAAGGCTTAGGCATGTTCAAACG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding 4277 human colon cancer-associated polypeptides, useful for preventing, diagnosing and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITCACTITCTACTITITTCATITIGITCTGTTCGAATTITITATAAGTATGTATACTT 2409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTGTAATCAGAATTTTTAGAAAGTATTTTGCTGATTTAAAAGGCTTAGGCATGTTCAAACG 2469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   colon cancer antigen; diagnosis; detection;
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1752 CCATAGACTAAGAATAAGAAGCATCATACTATAACTGAACACAATG 1797
                                                                                                                                                                                                                                Human colon cancer antigen encoding cDNA SEQ ID NO:196.
                    46 CCATAGACTAAGAATAAGAAGCATCATACTATAACTGAACACAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 417 BP; 118 A; 61 C; 65 G; 172 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.9%; Score 359; DB 22;
99.8%; Pred. No. 3.3e-122;
tive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rosen
                                                                                                                                                                                                                                                                                     colorectal carcinoma; chromosome X; ss.
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                                                                                                                         AAH33140 standard; cDNA; 417 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-2000; 2000WO-US26524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0157137.
                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barash SC,
                                                                                                                                                                                                                                                                   colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-235357/24
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                                                                                                                                                                                             03-SEP-2001
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                                                                                                                                                              AAH33140;
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Matches 40
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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              нитап; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
gene therapy; chromosome mapping; ss.
CCTGCAAAACTACTTATCACTCAGCTTTAGTTTTTCTAATCCAAGAAGGCAGGGAGTTA 2529
                                                                                                                                                                                                                                                                                                                                  AAAATATTTCTGAGTGGTAGTTTTTTGACAGGTAGACCATGTCTTATCTTGTTTCAAAAT 2649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 ARAATATTTCTGAGTGGTAGTTTTTTGACAGGTAGACCATGTCTTATCTTGTTTCAAAAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGCAAAACTACTTATCACTCAGCTTTAGTTTTTTCTAATCCAAGAAGGCAGGGCAGTTA 180
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                                                                                                                                                                   <u> ACCTTTTTGGTGCCAATGTGAATGTAAATGTTTTTATGTTTTTTCTGTGGATGA</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein 5' EST, SEQ ID NO: 29306.
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WPI; 2001-457603/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cancer; ulcer; HIV infection; human immunodeficiency virus; antinflammatory; antirheumatic; antiarthritic; immunosuppressive; antiaflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; Virucide; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidiabetic; cytostatic; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; genetic disease; haematopoietic disorder; platelet disorder; asthma; thrombocytopeania; osteoporosis; disorder; platelet disorder; asthma; thrombocytopeania; osteoporosis; disorder; platelet disorder; allergic nations musical manificial depotes; multiple sclerosis; depression; allergic nations.
                                                                                                                                                                            TGTTTAGAAATGCTGTTGCTTCAGGTTCTTAAAATCACTCAGCACTCCAACTTCTAATCA 4184
                                                                                                                                                                                                                              4185 AATTITIGGAGACTIAACAGCATTIGTCTGTGTTIGAACTATAAAAAGCACCGGATCTTT 4244
                                                                                                                                                                                                                                                                               TCCATCTAATTCCGCAAAAATTGATCATTTGCAAAGTCAAAACTATAGCCATATCCAAAT 4304
                                                                         CCATGAGTTGTGAAATTTAATGCACACGCTGATGTGGCTAACAAGGTTTATTTTAAGAAT 4124
                                                                                                                                         241 TCCATCTAATTCCGCAAAAATTGATCATTTGCAAAGTCAAAACTATAGCCATATCCAAAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                   Gaps
                                                                                                 0;
                                                                                        Length 315;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein encoding cDNA sequence SEQ ID NO:57.
 A; 65 C; 42 G; 112 T; 0 other;
                         Score 314; DB 21; I Pred. No. 1.1e-105;
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                       6.0%; Score 314; DB ilarity 100.0%; Pred. No. 1.1 Conservative 0; Mismatches
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AAH99222 standard; cDNA; 1129 BP.
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                CTTTTCCCCCTCCC 4318
                                                                                                                                                                                                                                                                                                                                            301 CTTTTCCCCTCCC 314
Sequence 315 BP; 96
                                    Similarity
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                                                  Matches 314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH99222;
                         Query Match
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AAM199166 to AAM199904 encode the human proteins given in AAW25225 to AAW25963. The proteins can have activities based on the tissues and cells they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; cardiant; cardiant; antianaemic; antiangaregant; haemostatic; uninerary; cardiavascular; antianaemic; antiallagregant; haemostatic; uninerary; antidlabetic; cytostatic; neuroprotective; antidlapersic; antiasthmatic; antidlabetic; cytostatic; neuroprotective; antidepressant; nootropic; antidlabetic; cytostatic; neuroprotective; antidepressant; nootropic; cardiabetic; cytostatic; neuroprotective; antidepressant; nootropic; cardiabetic; cytostatics; neuroprotective; antidepressant; nootropic; conding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, cheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, infections, autoimmunity, genetic diseases, haematopoietic disorders, cancer, multiple sclerosis, depression, chinitis, asthma, disbease, parkinson's disease, neurodegenerative and chinitis, asthma, disbease, meurolegenerative and chinitis, neurolegical disorders.
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iive 0; Mismatches 0;
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P-PSDB; AAM25281
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SEQ ID NO 3
LENGTH: 5232
TYPE: DNA
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
                   GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-617-053A-3
US-09-392-580-1
US-09-239-867-3
US-08-742-185-102
US-08-742-185-101
US-09-34-601-5
US-09-34-601-5
US-09-34-601-5
US-09-34-601-5
US-09-334-601-5
US-09-334-601-5
US-09-334-601-5
US-09-35-075-101-43
US-09-875-222-2
US-09-676-6108-2
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US-09-851-894A-3
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US-09-058-389A-12
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length: 2000000000
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GENERAL INFORMATION:

APPLICANT: Mackenile, Alexander E
APPLICANT: Mackenile, Alexander E
APPLICANT: Mackenile, Alexander E
APPLICANT: Mackenile, Alexander E
APPLICANT: Mackenile, Stephen
APPLICANT: Baird, Stephen
APPLICANT: WAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: 06/012, 971B
CURRENT FILING DATE: 1996-11-16
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER PILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTERQ for Windows Version 4.0
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                                                                                                                                                                        Sequence 3, Appll
Sequence 1, Appl
Sequence 9, Appll
Sequence 7, Appll
Sequence 616, App
Sequence 118, Appl
Sequence 11, Appl
                                                                                                                                651, App
3, Appli
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                        Sequence 5, Al
Sequence 33, Bequence 33, Sequence 33, Sequence 51, Sequence 55, Sequence 551, Sequence 3, Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAAAGGTGGACAAGTCCTATTTTCAAGAAGATGACTTTTAACAGTTTTGAAGGATCT
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US-09-611-781-12
US-09-058-389A-5
US-08-888A-5
US-08-888-497-33
US-09-352-230-33
US-09-613-133A-3
US-09-754-50-53
US-09-754-250-3
US-09-754-250-3
US-09-754-250-3
US-09-11-485-9
US-08-111-485-9
US-09-128-155-17
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iive 0; Mismatches
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; LOCATION: (4622)
... OTHER INFORMATION: n can be any nucleotide
US-09-212-971-3
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OTHER INFORMATION: n can be any nucleotide
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Best Local Similarity 100.
Matches 5232; Conservative
                                            6354
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oy Op	2341	TAGGGCCTTTTCACTTTCTACTTTTCATTTGTTCTTCGAATTTTTTATAAGTAT 2400
oy B	2401	GTATTACTTTTGTAATCAGAATTTTTAGAAAGTATTTTGCTGATTTAAAGGCTTAGGCAT 2460
Oy Dp	2461	GTTCAAACGCCTGCAAAACTACTTATCACTCTAGCTTTTGTTATTCTAATCCAAGAAGGCA 2520
9 Pp 93	2521 2521	GGGCAGTTAACCTTTTTGGTGCCAATGTGAAATGTAAATGATTTTATGTTTTTTCTGCTT 2580
oy Op	2581 2581	TGTGGATGAAAAATTTTCTGAGTGGTAGTTTTTTGACAGGTAGACCATGTCTTATCTTG 2640
O.Y.	2641	TITCAAAATAAGTATITCIGAITITGTAAAAIGAAAIAIAAAAIATGICTCAGATCITCC 2700
Oy Db	2701 2701	AATTAATTAGTAAGGATTCATCCTTAATCCTTGCTAGTTTAAGCCTGCCT
Oy Dp	2761 2761	ACTAAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGGTAAAAGT 2820
oy Ob	2821	AGAAGCATGTTTGTACACTGCTTGTAGTTATAGTGACGCTTTCCATGTTGAGATTCTCA 2880
Oy Op	2881	TATCATCTTGTATCTTAAAGTTTCATGTGAGTTTTTACCGTTAGGATGATTAAGATGTAT 2940
Oy Dp	2941	ATAGGACAAAATGTTAAGTCTTTCCTCTACCTACATTTGTTTTCTTGGCTAGTAATAGTA 3000
Ç, G	3001	GTAGATACTICTGAAATAAATGIICTCTCAAGATCCITAAAACCICTTGGAAAITATAAA 3060
Q Pp	3061	AATATTGGCAAGAAAAGAATAGTTGTTTAAATATTTTTTAAAAAAACACTTGAATAAG 3120
S G	3121	AATCAGTAGGGTATAAACTAGAAGTTTAAAAATGCCTCATAGAACGTCCAGGGTTTACAT 3180
Zy Gp	3181	TACAAGATTCTCACAACAAACCCATTGTAGAGGTGAAGGCATGTTACTACAGAGGA 3240
Sy Bp	3241	agtitgagagtaaaactgtaaaaaattatattttgttgtactttctaagagaagagta 3300
oy O	3301	TIGITAIGITCICCTAACITCIGITGAITACIACITTAAGIGAIAITCAITIAAAACAIT 3360
δ	3361	GCAAATTTATTTTATTTAATTTTCTTTTGAGATGGAGTCTTGCTTG

ACTTATCTTTATTTGTAATAATTTAGTCTGCTGATCAAAAGCATTGTCTTAATTTTTGAG **ATTTTTTTTTTTTTTTAGTAGAGACGGGGTTTCACCATGTTGGCCCAGGCTGGTATCAAAC** TCCTGACCTCAAGAGATCCACTCGCCTTGCCCTCCCAAAGTGCTGGGATTACAGGCTTGA ACTGCCCTGTTTCTGTTTTAGTATGTAAATCCTCAGTTCTTCACCTTTGCACTGTCTGCC **ACTTAGTTTGGTTATATAGTCATTAACTTTGAATTTGGTCTGTATAGTCTAGACTTTAAAT AATTGTTTTAACATAAGGCTTTTCCTGTTCTGGGAGCCGCACTTCATTAAAATTCTTCTA** q qq Dp QQ QQ a g ò g δ qq δy g δy g δy g οy g οy qq δλ qq δy QΩ ò g δ qq οy ŏ δ δ δ Óγ ò

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; OTHER INFORMATION: N at 4622 and 4633 can be A, US-08-800-929A-3
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                                                                              SOFTWARE: FastSED for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 5232; D
; Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 07891/009001
ELECOMMUNICATION:
TELEPHONE: 617-428-0200
TELEPHONE: 617-428-045
                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                 NAME: Bieker-Brady, Kristina REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                     IBM Compatible
                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 5232 base pairs
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Matches 5232; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   single
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                   OPERATING SYSTEM:
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                                                      TITCCIGCIACATITGGIIITITCCCCTGTCCCTTTGATTACGGGCTAAGGTAGGGTAAG 4620
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                                                                                                                         Sequence 3, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Liston, Peter
APPLICANT: Liston, Peter
APPLICANT: Tanny, Benjamin K
APPLICANT: Tanny, Benjamin K
APPLICANT: Tanny, Benjamin K
APPLICANT: Fratt, Christine
TITLE OF INVENTION: DETECTION AND MOI
TITLE OF INVENTION: IAPS AND NAIP FOI
TITLE OF INVENTION: IAPS AND NAIP FOI
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2: Clark & Elbing LLP
176 Federal Street
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Qy	1621	68
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Qy	1741	AATTGAAACCATAGACTAAGAATAAGAAGCATCATACTATAACTGAACACAATGTGT 1
Qy Db	1801	ATTCATAGTATACTGATTTAATTTCTAAGTGTAAGTGAATTAATCATCTGGATTTTTAT 1
Qy	1861	TCTTTTCAGATAGGCTT
Qy	1921	aaaaggaataaattgttccatgctggtg. 1
Qy	1981 1981	IGTTTTTAGAGGTTGGTTGTTTTTAGGATTCTGTCCATTTTC
Qy	2041	TITAAAGITATAAACACGTACITGTGCGAATTATTTTTTAAAGTGATTGCCATTTTTG 2
Qy	2101	AGCGTATTTAATGATAGATACTATCGAGCCAACATGTACTGACATGGAAAGATGTCA 2
Qy	2161	AAGATATGTTAAGTGTAAAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGATCA 222.
Qy	2221	AAGTATGTATGTTTTTAATATGCATAGAACAAAAGATTTGGAAAGATATACACCAAACTG 228
QY	2281	TIAAATGIGGITICICTICGGGGGGGGGGATTGGGGGGGGCCCCAGAGGGGTTITA 234
QY	2341	TAGGGCCTTTTCACTTTCTACTTTTTCATTTTGTTCTGTTCGAATTTTTTATAAGTAT 2400
QY	2401	GTATTACTITIGTAATCAGAAITTITAGAAAGTATTITGCTGAITTAAAGGCTTAGGCAT 246
Qy	2461	O O
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Qy	2581	TGTGGATGAAAAATTTTTGAGTGGTAGTTTTTTGACAGGTAGACCATGTCTTATCTTG 2:
Qy	2641	TTTCAAAATAAGTATTTCTGATTTTGTAAAATGAAATATAAAATATGTGTCTCAGATCTTCC 2700

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Petent No. 6300492
GENERAL INFORMATION:
APPLICANT: Kornelluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Tsang, Benjamin K
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine AND MODULATION
TITLE OF INVENTION: DETECTION AND MODULATION
TITLE OF INVENTION: DISEASE
FILLE OF INVENTION: DISEASE
FILLE OF INVENTION: DISEASE
FILLE REPERENCE: 07891/009003
CURRENT FILLING DATE: 2000-07-14
FRIOR FILING DATE: 1997-02-13
NUMBER: OF SEQ ID NOS: 17
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ZIP: 02110-2804
COMPUTER REAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Pred. No. 0
                                                                                                                                                                 07540/002001
                                                                                    APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
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                                                                                                                                                               REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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100.0%;
                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
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SEQUENCE CHARACTERISTICS:
LENGTH: 2540 base pairs
                                                                                                                                                                                                                                                                                                                                                                  Matches 2040; Conservative
                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: both
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Best Local Similarity
                                                                                                                                                                                                                                                                                           both
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US-08-511-485-3
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Oy 1741 TTTAATTGAAACCATAGAATAAGAAGCATGATACTATAACTGAACAGAATGTGT 1800	1741	OY 1801 ATTCATAGTATACTGATTTAATTTCTAAGTGAAGTGAAG	1861	DD 1861 TCTTTTCAGATAGGCTTACAAATGGAGCTTTCTGTATATAAATGTGGAGTTAGAGTTA 1920 QY 1921 ATCTCCCCAATCACATTGTTTTGTGTGAAAAAGGAATAAATTGTTCCATGCTGGTG 1980	Db 1921 ATCTCCCCAATCATAATTGTTTTGTGAAAAGGAATAAATGTTCCATGCTGGTG 1980 Oy 1981 GAAAGATAGATTGTTTTAGAGGTTGGTGTTGTTTTAGGATTCTTCT 2040	Db 1981 GAAAGATAGAGATTGTTTTAGAGGTTGGTTGTTGTTTTAGGATTCTGTCCATTTCT 2040 Qy 2041 T 2041	Db 2041 T 2041	E-SULT 7 S-09-392-580-1 Sequence 1, Application US/09392580 Patent No. 6087173	ENERAL INFORMATION: APPLICANT: C. Frank Bennett APPLICANT: Elizabeth J. Ackermann APPLICANT: Elizabeth J. Ackermann APPLICANT: CAN SERVICANT: ACKERMANN APPLICANT: CAN SERVICANT: CAN SERV	TILLE REFERENCE: RTS-0072 CURRENT APPLICATION NUMBER: US/09/392,580 WINDER FILING DATE: 1999-09-09	NOMBER OF SEQ ID NOS: 4/	0- 8	Query Match 38.0%; Score 1990; DB 3; Length 2540; Best Local Similarity 100.0%; Pred. No. 0;	MACCINES 2040; COUSELVALIVE U; MISMBCCNES I; INDELS U; Gaps U; QY I GAAAAGGTGGACAAGTCTATTTTCAAGAAGATGACTTTTAACAGTTTTGAAGGATCT 60 Dh I GAAAAGCGCCAACCAACTATTTTAAAGAACAACAACAACAACAACAACAACAACAACAACAAC	61 AAAACTTGTGACCTGCAGACATCAATAAGGAAGAAGAATTTGTAGAGGTTTP 61 AAAACTTGTGACCTGCAGACATCAATAAGGAAGAAGAATTTGTAGAAGGTTTP 61 AAAACTTGTGACACATCAATAACGAAGAAGAAATTTGTAGAAGGTTTP	121 TTAAAAACTTTTGCTAATTTTCCAAGTGGTAGTCCTGTTTCAGCATCACGCACG	181 GCAGGGTTCTTTATACTGGTGAAGGAGATACCGTGCGTGC	241 GTAGATAGATGCCAATATGGAGACTCAGCAGTGGGAGACACAGGGAAGGTTGCAAGTTGGAAGGTTGCAAGTTTGCAAGTTTCCCCAAAT

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             TTTAATTGAAACCATAGACTAAGAATAAGAAGCATCATACTATAACTGAACACAATGTGT
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APPLICANT: Robert G. Korneluk et al.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR
TITLE OF INVENTION: MALE FERTILITY
FILE REFERENCE: 07891/018002
CURRENT APPLICATION NUMBER: 60/073,001
PRIOR APPLICATION NUMBER: 60/073,001
PRIOR APPLICATION NUMBER: 60/073,001
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.4%; Score 1588; D
100.0%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09239867
Patent No. 6331412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 1588; Conservative
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US-09-239-867-3
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TGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAATAT 1020 540 099 720 720 840 840 900 900 960 240 240 300 300 360 360 420 420 480 480 540 900 009 999 780 780 180 180 GITITGGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTTCTGATAGGAAT CTGTTAGAACAGAAGGGACAAGAATATATAAAACAATATTCATTTAACTCATTCACTTGAG GTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAAGTATCCCCCAAAT ATCCAGAATGGTCAGTACAAAGTTGAAAACTATCTGGGAAGCAGAGATCATTTTGCCTTA TACTACACAGGTATTGGTGACCAAGTGCAGTGCTTTTGTTGTGGTGGAAAAATT TGGGAACCTTGTGATCGTGCCTGGTCAGAACACAGGCGACACTTTCCTAATTGCTTCTTT TTCCCAAATTCAACAAATCTTCCAAGAAATCCATCCATGGCAGATTATGAAGCACGGATC TTCCCAAATTCAACAAATCTTCCAAGAAATCCATCCATGGCAGATTATGAAGCACGGATC TATGCTTTAGGTGAAGGTGATAAAGTAAAGTGCTTTCACTGTGGAGGAGGGCCTAACTGAT TTAAAAACTTTTGCTAATTTTCCAAGTGGTAGTCCTGTTTCAGCATCAACACTGGCACGA GCAGGGTTTCTTTATACTGGTGAAGGAGATACCGTGCGGTGCTTTAGTTGTCATGCAGCT TGCAGATTTATCAACGGCTTTTATCTTGAAAATAGTGCCACGCAGTCTACAAATTCTGGT TCAGACACCATATACCCGAGGAACCCTGCCATGTATAGTGAAGAAGCTAGATTAAAGTCC TITCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGAGAGTTAGCAAGTGCTGGACTC TTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTTGCAAGAGCTGGATTT 1081 ò

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TELECOMMUNICATION INFORMATION
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MOLECULE TYPE: DNA (genomic)
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CITY: Lexington
THANS: Massachusetts
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                            TELEPHONE:
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APPLICANT: Page, David C.
APPLICANT: Page, David C.
APPLICANT: Saxena, Richa
APPLICANT: Hawkins, Trevor
APPLICANT: Heawkins, Trevor
APPLICANT: Reeve, Mary Pat
TITLE OF INVENTION: DA2: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
WUWBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STRET: Laxington
CITY: Lexington
STATE: Massachusetts
                                                                            1141 ATCTTCCAAAATCCTATGGTACAAGAAGCTATACGAATGGGGTTCAGTTTCAAGGACATT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,185
FILING DATE: 30-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/690,734
FILING DATE: 31-JUL.1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/690,734
APPLICATION NUMBER: US 08/690,734
APPLICATION NUMBER: US 08/690,734
APPLICATION NUMBER: US 08/690,734
APPLICATION NUMBER: US 08/310,429
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ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH194-07A2
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APPLICANT: Page, David C.
APPLICANT: Page, Rebe
APPLICANT: Saxena, Richa
APPLICANT: Hawkins, Trevor
APPLICANT: Reeve, Mary Pat
TITLE OF INVENTION: DAZ: A GENE FAMILY ASSOCIATED WITH AZOOSPERMIA
NUMBER OF SEQUENCES: 102
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
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                                                                                                                                                                                                                                                                          Length 40328;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,185
FILING DATE: 30-C1-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/690,734
FILING DATE: 31-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,429
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32-227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5015 GACCATCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAA 5057
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Two Militia Drive
                                                                                                                                                                                                                                                                          Query Match 2.0%; Score 103; DB 3; Best Local Similarity 100.0%; Pred. No. 3.3e-31; Matches 103; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: WH194-07A2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-742-185-101/c; Sequence 101, Application US/08742185; Patent No. 6020476; DENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 43795 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 102
SEQUENCE CHARACTERISTICS:
LENGTH: 40328 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-742-185-102
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Query Match
Best Local Similarity
Matches 81; Conserv
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CRGANISM: Human
US-09-740-035-3
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US-07-869-933-31
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US-09-740-035-3
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TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE OF INVENTION: AND USES THEREOF
FILE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US 60/091,650
EARLIER PELLING DATE: 1998-09-03
EARLIER FILING DATE: 1998-07-02
EARLIER FILING DATE: 1997-08-04
NUMBER OF SED ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH::152331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23907 CCTGATTGAATGTGTGTGTGAACTGACTTTAAGTAATCAGGATTGAATTCCATTAGCAT 23848
                                                                                                                                1567 CCTGATTGAATGTGTGTGTGAACTGACTTTAAGTAATCAGGATTGAATTCCATTAGCAT 1626
                                                                                                            4955 GCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCAGGTCACGAGGTCAGGAGATCGA 5014
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                                    Length 43795;
                                                                       Indels
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                                                                                                                                                                                      5015 GACCATCCTGGCTAACACGGTGAAACCCCGTCTCTACTAAAAA 5057
                                  Score 103; DB 3; I
Pred. No. 3.3e-31;
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100.0%; Pred. No. 1.5e-23;
tive 0; Mismatches 0;
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APPLICANT: Kapitonov, Dmitri
APPLICANT: Wapitonov, Dmitri
TITLE OF INVENTION: NOVEL SIALYLTRANSFERASES
FILE REFERENCE: VCUIP-6
CURRENT APPLICATION NUMBER: US/09/334,601
CURRENT APPLICATION NUMBER: 1999-06-17
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
                   2.0%; Scort No. 100.0%; Pred. No. ... 0; Mismatches
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US-09-128-155-16/c
; Sequence 16, Application US/09128155
; Patent No. 6117654
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COTHER INFORMATION: n = A,T,C or G
US-09-128-155-16
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; Sequence 5, Application US/09334601
; Patent No. 6280989
                                                      Best Local Similarity 100.
Matches 103; Conservative
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Matches 83; Conserv
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US-08-742-185-101
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                                    Query Match
Best Local
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GENERAL INFORMATION:
APPLICANT: YE, Jane et al
APPLICANT: YE, Jane et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: UGES THEREOF
TITLE OF INVENTION: UGES THEREOF
TITLE OF INVENTION: UGES THEREOF
CURRENT APPLICATION NUMBER: US/09/740,035
CURRENT FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: TSOLATION, CHARACTERIZATION, AND USE OF TITLE OF INVENTION: TSOLATION, CHARACTERIZATION, AND USE OF TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR TITLE OF INVENTION: IMMUNOGLOBULIN NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS: ADDRESSE: Foley & Lardner STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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                                                                                           5089 CCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGAATGGTGTGAACCCGGGAGGCAG 5148
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Pred. No. 6.2e-20;
       Length 3494;
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COUNTRY: USA
ZIP: 2313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FTUING DATE: 19920416
1.5%; Score 81; DB 4; L
100.0%; Pred. No. 1.5e-22;
tive 0; Mismatches 0;
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                                                                                                                                                                                          5149 AGCTTGCAGTGAGCCGAGATC 5169
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APPLICANT: KINET, Jean-Pierre
                                                                                                                                                                                                                                     28 AGCTTGCAGTGAGCCGAGATC
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Best Local Similarity 100.
Matches 74; Conservative
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                                                  Conservative
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GENERAL INFORMATION:
APPLICANT: Kinct et al.
APPLICANT: Kinct et al.
TITLE OF INVENTION: Isolation, characterization, and use of the human beta
TITLE OF INVENTION: subunit of the high affinity receptor for
TITLE OF INVENTION: immunoglobulin E.
TITLE OF INVENTION: immunoglobulin E.
TITLE OF INVENTION: immunoglobulin E.
CURRENT APPLICATION NUMBER: US/09/103,663D
CURRENT APPLICATION NUMBER: 07/869,933
EARLIER APPLICATION NUMBER: 07/869,933
EARLIER FILING DATE: 1992-04-16
NUMBER OF SEQ ID NOS: 35
SOFTARE: Patentin Ver. 2.1
LENGTH: 11298
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                                                                                                                                                                                                                                                                          ; LOCATION: join(456..511, 1381..1510, 2026..2160, 4475..4531, ; LOCATION: 5079..5237, 5640..5738, 7224..7319)
US-08-201-879A-2
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Patent No. 6451763
GENERAL INFORMATION:
APPLICANT: Tombran-Tink, Joyce
APPLICANT: Steele, Fintan R
APPLICANT: Chader, Gerald J
APPLICANT: Becerra, Sofia P
APPLICANT: Johnson, Lincoln V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31, Application US/09103663D Patent No. 6171803
                         SEQUENCE CHARACTERISTICS:
LENGTH: 11298 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOCLGY: linear
ORIGINAL SOURCE:
ORGANISM: Home sapiens
     INFORMATION FOR SEQ ID NO: 2:
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Best Local Similarity 100.C
Matches 70; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 10835 TACTAAAAA 10844
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US-08-520-373D-4
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Sequence 2, Application US/08201879A
Fatent No. 5807988
GENERAL INFORMATION:
APPLICANT: KINET, Jean-Pierre
APPLICANT: AJOUVIN, Marie-Helene
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR TITLE OF INVENTION: IMMUNOGLOBULIN E
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LAIGHER
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Best Local Similarity 100.0%; Pred. No. 2.4e-18;
Matches 70; Conservative 0; Mismatches 0; Indels
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ZIP: 2000-5109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/201,879A
FILING DATE: 16-APR-1994
PRIOR APPLICATION NUMBER: US 07/869,933
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/03419
FILING DATE: 16-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7689
                                                                          40399/154 NIHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 40399/234/NIHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                   REGISTRATION NUMBER: 40395
REFERENCE/DOCKET NUMBER: 40395
TELECOMMUNICATION INFORMATION:
TELEPAN: (703)836-9300
TELESA: 899149
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 11298 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                29,768
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
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TELEX: 904136
                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: homo sapien
STRAIN: FCRI beta
                         NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                        TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 10835 TACTAAAAA 10844
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### APPLICANT: Rodriguez, Ignacio R
### TITLE OF INVENTION: RETRIAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
FILE REPERENCE: 2026-4203031
CURRENT APPLICATION NUMBER: 08/209-99
PRIOR RELIGNED DATE: 1995-08-29
PRIOR RELIGNED DATE: 1995-01-25
PRIOR RELIGNED DATE: 1995-01-25
PRIOR PILING DATE: 1992-06-04
PRIOR RELIGNED DATE: 1992-06-04
PRIOR RELIGNED DATE: 1992-06-04
PRIOR RELIGNED DATE: 1992-06-04
PRIOR RELIGNED DATE: 1992-09-24
PRIOR PILING DATE: 1992-09-24
PRIOR PILING DATE: 1992-09-24
PRIOR RELIGNED DATE: 1993-09-24
PRIOR PILING DATE: 1993
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Search completed: November 10, 2002, 04:46:12 Job time : 1269 secs

Db 12945 TACTAAAAA 12953

Perfect score:

Run on:

Sequence:

Word size :

Searched:

Database :

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APPLICANT: MCKCRAIL, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baria, Stephen
APPLICANT: Tang, Benjamin K
APPLICANT: Trang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009004
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009004
CURRENT PAPLICATION NUMBER: US 09/617,053
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR APPLICATION NUMBER: US 08/800,929
SRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 5232
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US-09-764-877-3833

US-09-263-959-295

US-09-764-869-1489

US-09-764-860-1075

US-09-764-869-2259

US-09-764-869-2259

US-09-764-869-2259

US-09-764-877-3979

US-09-764-877-3979

US-09-764-877-3979

US-09-860-1018

US-09-860-1018

US-09-860-107-3950

US-09-954-456-292

US-09-954-456-292

US-09-954-456-292

US-09-954-456-293

US-09-964-456-293

US-09-964-456-293

US-09-880-107-1542

US-09-880-107-1542

US-09-880-107-105-105-1065
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US-09-764-869-1556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09974592
Patent No. US20020120121A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Korneluk, Robert
APPLICANT: MacKenzie, Alexa
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 739
1400
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9745
12145
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18385
22484
43058
43058
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522168
110095
618659
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: variation
LOCATION: 4623
OTHER INFORMATION: n
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LOCATION: 4622
  Query Match
Best Local Simi
Matches 5232;
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US-09-974-592-3
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    FEATURE:
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Sequence 154, Appl
Sequence 32, Appl 1
Sequence 421, Appl
Sequence 421, Appl 1
Sequence 1, Appl 1
Sequence 1, Appl 1
Sequence 7428, Ap
Sequence 643, Ap
Sequence 643, Ap
Sequence 1433, Ap
Sequence 1433, Ap
Sequence 1434, Ap
Sequence 1844, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Appli
Sequence 13853, A
Sequence 30419, A
Sequence 2426, Ap
Sequence 61, Appl
                                                                                                         (without alignments)
11318.521 Million cell updates/sec
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                                                                                            November 10, 2002, 00:05:56; Search time 164 Seconds
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/cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*
               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-974-592-3
US-09-864-761.13853
US-09-864-761.30419
US-09-764-877-2426
US-09-764-877-2426
US-09-962-832-154
US-09-962-832-154
US-09-795-688-421
US-09-795-688-421
US-10-014-502-3
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US-09-764-847-1844
US-09-764-847-1847
US-09-867-701-8277
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US-09-867-701-7428
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US-09-795-686-1
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                                                                                                                                                                                                                                                                                                                                                                                            Published_Applications_NA:*
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                                                                  OM nucleic - nucleic search, using sw model
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length: 2000000000
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Match Length
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3833, Ap 1489, App 11075, Ap 11075, Ap 2258, Ap 2258, Ap 2258, Ap 3979, Ap 3979, Ap 31018, Ap

Sednence Sed

r 60	A 120 A 120	A 180 180	r 240 240	r 300 300	r 360 360	A 420 A 420	A 480 A 480	c 540 540	009 p	r 660 660	T 720 T 720	T 780 † T 780 ·	c 840 840	т 900 1 т 900	r 960 960	r 1020 1020	G 1080 G 1080	2 1140 1140
TAACAGTTTTGAAGGATC	TTGTAGAAGAGTTTAATAGA 	CAGCATCAACACTGGCACGA 	CCTTTAGTTGTCATGCAGCT	ACACAGGAAAGTATCCCCAAAT 	CACGCAGTCTACAAATTCTGGT	CAGAGATCATTTGCCTT 	rgggcaggttgtagatat) 	ragaagctagattaaagtcc 	STAGCAAGTGCTGGACT 	GTGGTGGAAAACTGAAAAAT 	CTTTCCTAATTGCTTCTT 	GCTGTGAGTTCTGATAGGAA! 	AGATTATGAAGCACGGAT	CAGCTTGCAAGAGCTGGATT: 	GTGGAGGAGGCTAACTGAT 	STATCCAGGGTGCAAATAT 	TTAACTCATTCACTTGAG 	PAGAAGAATTGATGATACC
TCAAGAGAAGATGACTTT	aataaggaagaagaat 	GTAGTCCTGTTT 	3GAGATACCGTGCGG7 3GAGATACCGTGCGG7	AGCAGTTGGAAG! 	CTTGAAAATAGTGC 	IGAAAACTATCTGGGAAGCAGAG 	AGACTATCTTTGAGAACT(CTGCCATGTATAGTG	rcacctaacccaagagagtagc 	CAAGTGCAGTGCTTTTGTTGT 	GTCAGAACAGGCGACACTTTC 	CGAAGTGAATCTGAT 	CCAAGAATCCATCCATGGC 	CAGTTAACAAGGAG 	AAAGTGCTTTCACT	GGAACAACATGCTAAATGG' 	CAGAAGGGACAAGAATATATAAACAATATTCAT' 	BAAACACCATCACTAACT
aaaaggtggacaagtcctattt	CTTGTGTACCTGCAGACAI 	TAAAAACTTTTGCTAATTTTCCAAGTG 	AGGGTTCTTATACTGGTGAA(AGATAGATGGCAATATGGAGACTC 	CAGATTATCAACGGCTTTATAT 	CCAGAATGGTCAGTACAAAGTTC 	CAGGCCATCTGAGACACATGC/ 	AGACACCATATACCCGAGGAACC 	CAGAACTGGCCAGACTATGCT 	PACACAGGTATTGGTGAC 	SAACCTTGTGATCGTGCCTG 	TTGGGCCGGAATCTTAATATTC 	CCCAAATTCAACAAATCTTCC 	TACTTTGGGACATGGATATACT(CCTTTAGGTGAAGGTGATAAAG1 	GAAGCCCAGTGAAGACCCTTGGGAACAACAT 	TTAGAA TAGAA	GTGTCTGGTAAGAACTACTGAGAAACACCATCACTAACTA
1 GA	61 AAAA(121 TTR 121 TTR	181 GC	241 GTA 241 GTA	301 TGC 	361 ATC 361 ATC	421 GAC 421 GAC	481 TCZ 481 TCZ	541 TTT 541 TTT	601 TACT 601 TACT	661 TGG 160	721 GTTT: 721 GTTT	781 TTC 781 TTC	841 TTT 841 TTT	901 TAT 901 TAT	961 TGC 961 TGC	1021 CTG1 1021 CTG1	1081 GAC 111 1081 GAC
qq	Oy Dp	Oy Dp	O.Y	oy Dp	Oy Dp	Qy Db	Qy Db	Oy Db	oy Ob	yo da	Oy Db	oy Dp	QY Db	Qy Db	Oy Db	Qy Dp	Qy	े. के वि <i>्र</i>

AAGATATGTTAAGTGTAAAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCAGATCA ATCTTCCAAAATCCTATGGTACAAGAAGCTATACGAATGGGGTTCAGTTTCAAGGACATT ACTIGIAAACAAIGIGCIGAAGCAGIIGACAAGIGICCCAIGIGCIACACAGICAIIACI TITAATIGAAACCATAGACTAAGAATAAGAAGCATCATACTATAACTGAACACAATGIGT TTTAAAGTTATAAACACGTACTTGTGCGAATTATTTTTTTAAAGTGATTTGCCATTTTTG AAAGCGTATTTAATGATAGAATACTATCGAGCCAACATGTACTGACATGGAAAGATGTCA **AAGAAAATAATGGAGGAAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAGGTT** CTGGTTGCAGATCTAGTGAATGCTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT TCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTAAAGGCGCCTGCAAGAGGAGGAGCTT Db Qy QQ O. Db oy Oy d do Db Qy Db Qy Db QY Db δŽ do Qy QY Db QY Dp δ Oy Db δ ద S Q οŽ

Db 3	2y 3			oy d			OY 3	Qy 3		QY 3							Qy 4 Db 4	Qy 4 4	4 4 do	0y 4
2221 AAGTAIGITITITAATAIGCATAGAACAAAAGATITGGAAAGATAIACACCAAACIG 2280 	81 TTAAATGTGGTTTCTCTTCGGGGAGGGGGGATTGGGGGGGG	81 TTAAATGTGGTTTCTCTTCGGGGGGGGGGATTGGGGGGGG	2341 TAGGGGCCTTTTCACTTTCTACTTTTTCATTTTGTTCCGAATTTTTTTATAGGTAT 2400 2341 TAGGGGCCTTTTCACTTTCTACTTTTTTTATAGTTCTGTTCGAATTTTTTATAGGTAT 2400	2401 GTATTACTTTTGTAATCAGAATTTTTAGAAAGTATTTTGCTGATTTAAAGGCTTAGGCAT 2460	2401 GTATTACTTTTGTAATCAGAATTTTTAGAAAGTATTTTGCTGATTTAAAGGCTTAGGCAT 2460	2461 GTTCAAACGCCTGCAAAACTACTTATCACTCAGCTTTAGTTTTTCTAATCCAAGAAGGCA 2520 	25	G 264 264	1 TITCAAAATAAGTAITICTGAITITGTAAAATGAAATAIAAAATAAATTGTCTGAGAICTICC 270	01 AATTAATTAGTAAGGATTCATCCTTAATCCTTGCTAGTTTAAGCCTGCCT	CTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGGTAAAAGT 282 	CACTGCTTGTAGTTATAGTGACAGCTTTCCATGTTGP 	2881 TATCATCTTGTATCTTAAAGTTTCATGTGAGTTTTACCGTTAGGATGATTAAGATGTAT 2940 	2941 ATAGGACAAAATGTTAAGTCTTTCCTCTACCTACATTTGTTTCTTGGCTAGTAATAGTA 3000 	3001 GTAGATACTTCTGAAATAAATGTTCTCTCAAGATCCTTAAAACCTCTTGGAAATTATAAA 3060 	3061 AATATTGGCAAGAAAGAAGAATAGTTGTTTAAATATTTTTTAAAAACACTTGAATAAG 3120 	3121 AATCAGTAGGTATAAACTAGAAGTTTAAAAATGCCTCATAGAACGTCCAGGGTTTACAT 3180 	3181 TACAAGATTCTCACAACAACCCATTGTAGAGGTGAGTAAGGCATGTTACTACAGAGGAA 3240 	3241 AGTTTGAGAGTAAAACTGTAAAAATTATATTTTGTTGTACTTTCTAAGAGAAGAGTA 3300 	3301 TIGITATGITCTCCTAACITCTGTTGATTACTACTTTAAGTGATATTCATTTAAAAACAIT 3360
oy Dp	Qy	q	Oy Op	Οy	qq	Qy Dp	oy Op	Qy	Qy Dp	do Oy	Oy Op	Qy Dp	Qy Dp	ço Qo	oy O	ço Qo	oy gp	Qy Dp	Oy Dp	οy

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1332 AGAGATTAGTACTGAAGAGCAGCTAAGGCGCCTGCAAGAGGAGAAAGCTTTGCAAAATCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 TATGGATAGAAATATTGCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1452 ATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACTTTCAAGCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    346 ATGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACAAGTATTTCAAGCAAAA
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-08-03
PRIOR PLING DATE: 2000-08-03
PRIOR PLING DATE: 2000-10-04
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2001-01-30
PRIOR SPILING DATE: 2001-01-
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OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
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100.0%; Pred. No. 1.5e-150;
tive 0; Mismatches 0;
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-864-761-13853
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LENGTH: 489
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                                                  ACTTATCTTTATTTGTAATATTTAGTCTGCTGATCAAAAGCATTGTCTTAATTTTTGAG
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Sequence 13853, Application US/09864761
Sequence 13853, Application US/09864761
Sequence 13853, Application US/09864761
Septent No. US20020048763A1
SEMBRAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUANN GENOME-DERIVED SINGLE EXON NUCLEIC PRINTED OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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CURRENT FILING DATE: 2001-05-23
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CTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN ADULT LIVEK, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN B1474, SIGNAL = 1.8

OTHER INFORMATION: NT HIT: U32974.1, EVALUE 4.00e-78

OTHER INFORMATION: SWISSPROT HIT: P98170, EVALUE 7.00e-17

OTHER INFORMATION: EST_HUMAN HIT: A1628066.1, EVALUE 5.00e-68
US-09-864-761-30419
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCOODS
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEO ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                               Length 148;
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APPLICANT: Wang, Peijing Jeremy
APPLICANT: Wang, Peijing Jeremy
APPLICANT: Wang, Peijing Jeremy
APPLICANT: Page, David C.
FILLE REFERENCE: 0399.2007-002
CURRENT APPLICATION NUMBER: 05/09/801,574
CURRENT FILING DATE: 2001-03-07
PRIOR FILING DATE: 2000-03-07
PRIOR FILING DATE: 2000-01-03
PRIOR FILING DATE: 2000-01-03
PRIOR FILING DATE: 2000-01-03
NUMBER OF SEQ ID NOS: 90
                                                                                                                                             Query Match

2.8%; Score 148; DB 10;
Best Local Similarity 100.0%; Pred. No. 7.4e-42;
Matches 148; Conservative 0; Mismatches 0;
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Patent No. US20020147140A1
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Best Local Similarity 100.
Matches 89; Conservative
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LENGTH: 194
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                                                                                                          106 TCTTGATTTTTCAGGGTATTAGCTGTATTATCCATTTTTTTACTGTTATTTAATTGAAA 47
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OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
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ORGANISM: Homo sapiens
FEATURE:
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LENGTH: 148
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Db 110231 AAAATTAGCCGGGCGTGGTGGCGGGCGCCCTGTAGTCCCCAGCTACTCGGGAGGCTGAGGCA 110290
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100.0%; Pred. No. 2.5e-17;
Live 0; Mismatches 0; Indels
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Patent No. US20020045577a1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefanson, Hreinn
APPLICANT: Stefanson, Hreinn
TILE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
TILE DE INVENTION: HUMAN SCHIZOPHRENIA GENE
CURRENT APPLICATION NUMBER: US/09/795,668
CURRENT FILING DATE: 2001-02-28
PRIOR PILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FaatSEQ for Windows Version 4.0
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Fatent No. US200200949541
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefanson, Hreinn
APPLICANT: Steinthorsdottir, Valgerdur
TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2245.2005-001
CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT APPLICATION NUMBER: US 09/515,715
FRIOR APPLICATION NUMBER: US 09/515,715
FRIOR APPLICATION NUMBER: US 09/515,715
STORMER FLING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 1531
SOFTWARE: FastSEQ for Windows Version 4.0
: EDNGTH: 401
                                                                     ; LOCATION: (1)...(203654)
; OTHER INFORMATION: n = A,T,C or G
US-09-820-905-3
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Matches 77; Conservative
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Matches 76; Conservative
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ORGANISM: Homo sapiens
                                                  NAME/KEY: misc_feature
       ORGANISM: HUMAN
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Sequence 3, Application US/09820905
Sequence 3, Application US/09820905
Sequence 3, Application US/0020142938A1
Sequence 3, Application US/0020142938A1
GENERAL INFORMATION:
APPLICANT: Yan, Chunhua
APPLICANT: Yan, Chunhua
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/820,905
CURRENT APPLICATION NUMBER: 2001-03-30
NUMBER OF SEQ ID NOS: 5
NUMBER OF SEQ ID NOS: 5
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                                                                                                                                                                 Length 53542;
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2.2e-18;
                                                                                                                                                          Query Match 1.6%; Score 85; DB 10; I
Best Local Similarity 100.0%; Pred. No. 1.1e-20;
Matches 85; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 61
LENGTH: 53542
                                                                                                                                                                                                                                                                                                                                                                                          Db 47650 GGAGAATGGTGTGAACCCGGGAGGC 47674
                                                                                                                                                                                                                                                                                                                                                  5122 GGAGAATGGTGTGAACCCGGGAGGC 5146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 154, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
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                                                                                          ; ORGANISM: Homo sapiens
US-09-801-574-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
US-09-962-832-154
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LENGTH: 203654
                                                                       TYPE: DNA
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RESULT 12
US-09-795-686-1/c
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APPLICART: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOOLOSBOLV
CURRENT APPLICATION NUMBER: US/10/014,502
CURRENT APPLICATION NUMBER: 09/740,035
PRIOR PILING DATE: 2001-12-14
PRIOR PILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 19736
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                                                                                                                                                                  4983 GAGGCAGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCC 5042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5066 TTAGCCGGCCGTGGTGGCGGCGCCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAG
                                                                                                                            Gaps
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                                                                                 Length 401;
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                                                                                 Query Match 1.5%; Score 76; DB 10; Length 40 Best Local Similarity 100.0%; Pred. No. 2.5e-17; Matches 76; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 7.3e-17;
tive 0; Mismatches 0;
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Patent No. US20020045577A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefinthorsdottir, Valgerdur
APPLICANT: Guldher, Jeffrey R.
ITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2004-001
CURRENT APPLICATION WUMBER: US/09/795,668
CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: US 09/515,716
PRIOR FILING DATE: 2000-02-28
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SOFTWARE: FastSEQ for Windows Version 4.0
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; Patent No. US20020137184A1
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Best Local Similarity 100.C
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CORGANISM: Homo sapiens
US-10-014-502-3
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ORGANISM: Homo sapiens
FEATURE:
                     ; ORGANISM: Homo sapiens US-09-795-686-421
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LENGTH: 1503841
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US-10-014-502-3
; TYPE: DNA
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DD 1501676 CCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGATGGTGTGAATCGCGGAGGCAG 1501617
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100.0%; Pred. No. 9.1e-17;
tive 0; Mismatches 0; Indels 0;
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Patent No. US20020094954A1
GENERAL INFORMATION:
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansson, Hreinn
APPLICANT: Stefansward
TILE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
FILE REFERENCE: 2345.2005-001
CURRENT APPLICATION NUMBER: US/09/795,686
CURRENT APPLICATION NUMBER: US/09/795,686
PRIOR PILING DATE: 2001-02-28
PRIOR PILING DATE: 2000-02-28
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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OTHER INFORMATION: d-a or g or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)

OTHER INFORMATION: h-a or c or t/u
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LOCATION: (1)...(1531)
COTHER INFORMATION: r=g or a
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: y=t/u or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: m=a or c
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: k=g or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: k=g or t/u
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OTHER INFORMATION: w-a or t/u
NAME/KEY: misc.feature
LOCATION: (1)...(1531)
OTHER INFORMATION: b-q or c or
NAME/KEY: misc.feature
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Best Local Similarity 100.
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                        LOCATION: (1)...(1531)
OTHER INFORMATION: s=g or
NAME/KEY: misc_feature
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LOCATION: (1)...(1531)
OTHER INFORMATION: r=g or
NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
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4956 CCTGTAATCCCAGCACTTTGGGAGGCTGAGGCAGGTGGATCACGAGGTCAGGAGATCGAG 5015
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APPLICANT: Rosen et al.
TITLE DF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERBNCE: PA113
CURRENT APPLICATION NUMBER: US/09/764,887
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION OF ENGLOSE CONSULT PALM OF FILE WIMPER OF SEQ ID NOS: 658
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                           APPLICANT: Jones, Nobert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REPERENCE: 2.01021.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7428
LENGTH: 362
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1.3e-15;
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100.0%; Pred. No. 3e-15;
tive 0; Mismatches 0
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                                                                                                           ; Sequence 7428, Application US/09867701
; Patent No. US20020132237A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 643, Application US/09764887 Patent No. US20020042096A1
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Best Local Similarity 100.0
Matches 70; Conservative
                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
  3892 AACCCGGGAGGC 3903
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CORGANISM: Homo sapiens
US-09-764-887-643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapien
US-09-867-701-7428
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208 AGCCGAGATC 217
                                                                 RESULT 14
US-09-867-701-7428
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US-09-764-887-643
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LENGTH: 281
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Batent No. US20020147140A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005

CURRENT APPLICATION NUMBER: US/09/764,877

CURRENT APPLICATION WINDER: US/09/764,877

FILO APPLICATION DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031

SOFTWARE: Patentin Ver. 2.0
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9.1e-17;
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                                                                                                                                                                                                                                                                 LOCATION: (1)...(1531)
OTHER INPORMATION: w=a or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INPORMATION: b=g or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
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OTHER INFORMATION: d-a or g or t/u
MANE/KE: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (1)...(1531)
OUTHER INFORMATION: h-a or c or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
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LOCATION: (1)...(1531)
OTHER INFORMATION: k=g or t/u
NAME/KEY: misc_feature
LOCATION: (1)...(1531)
OTHER INFORMATION: s=g or c
NAME/KEY: misc_feature
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OTHER INFORMATION: v=a or g or
LOCATION: (1)...(1531)
OTHER INFORMATION: y=t/u or c
NAME/KEY: misc_feature
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                                                               LOCATION: (1)...(1531)
OTHER INFORMATION: m-a or c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens US-09-764-877-2432
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US-09-764-877-2432
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12572.445 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Pending_Patents_NA_Main:*

1: /cgn2_6/ptodata/2/pna/USOR_COMB.seq:*
2: /cgn2_6/ptodata/2/pna/USOR_COMB.seq:*
3: /cgn2_6/ptodata/2/pna/USOR_COMB.seq:*
4: /cgn2_6/ptodata/2/pna/USOR_COMB.seq:*
5: /cgn2_6/ptodata/2/pna/USOB_COMB.seq:*
6: /cgn2_6/ptodata/2/pna/USOB_COMB.seq:*
7: /cgn2_6
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2 6/ptodata/2/pna/US6000_COMB.s 2-6/ptodata/2/pna/US6001_COMB.s 2-6/ptodata/2/pna/US6001_COMB.s 2-6/ptodata/2/pna/US6004_COMB.s 2-6/ptodata/2/pna/US6006_COMB.s 2-6/ptodata/2/pna/US6006_COMB.s 2-6/ptodata/2/pna/US6006_COMB.s 2-6/ptodata/2/pna/US6009_COMB.s 2-6/ptodata/2/pna/US6010_COMB.s 2-6/ptodata/2/pna/US6011_COMB.s 2-6/ptodata/2/pna/US6011_COMB.s 2-6/ptodata/2/pna/US6011_COMB.s 2-6/ptodata/2/pna/US6011_COMB.s 2-6/ptodata/2/pna/US6011_COMB.s 2-6/ptodata/2/pna/US6011_COMB.s 2-6/ptodata/2/pna/US6011_COMB.s 2-6/ptodata/2/pna/US6011_COMB.s 2-6/ptodata/2/pna/US6011_COMB.s 2-6/ptodata/2/pna/US6011_COMB.s 2-6/ptodata/2/pna/US6011_COMB.s 2-6/ptodata/2/pna/US6011_COMB.s 2-6/ptodata/2/pna/US6011_COMB.s 2-6/ptodata/2/pna/US6011_COMB.s 2-6/ptodata/2/pna/US6012_COMB.s 2-6/ptodata/2/pna/US6012_COMB.s 2-6/ptodata/2/pna/US6012_COMB.s	
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 3, Appli	Sequence 3044, Ap	Sequence 3044, Ap	Sequence 231, App	Sequence 38, Appl	Sequence 1, Appli	Sequence 25, Appl	Sequence 25, Appl	Sequence 3, Appli	_	Seguence 3, Appli	Sequence 3, Appli	Sequence 900, App	Sequence 219, App	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 218, App	Sequence 274, App	Sequence 1, Appli
	ΠD	S US-09-974-592-3	PCT-US01-01324-3044		S US-09-672-717-231	5 US-09-964-899-38	PCT-US00-00583-1	PCT-US02-11757-25	PCT-US02-11758-25	US-08-576-956-3	US-08-576-956A-3	US-09-011-356-3	4 US-09-011-356-3	US-09-023-655-900	US-09-053-375B-219	5 US-09-201-932-3	5 US-09-201-932-3	5 US-09-201-936-3	5 US-09-654-743-3	5 US-09-672-717-218	3 US-10-007-926A-274	9 US-10-070-789-1
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dЮ	Ouery Match	100.0	48.0	48.0	43.5	38.7	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0	38.0
	Score	5232	2511	2511	2278	2027	1990	1990	1990	1990	1990	1990	1990	1990	1990	1990	1990	1990	1990	1990	1990	1990
	Result No.	П	7	m	4	5	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21

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APPLICANT: Korneluk, Robert G
APPLICANT: MacKenzie, Alexander E
APPLICANT: MacKenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Brand, Benjamin K
APPLICANT: Pratt, Christine
ITILE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
ITILE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
ITILE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009004
CURRENT APPLICATION NUMBER: US/09/974,592
CURRENT APPLICATION NUMBER: US 09/617,053
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
Sequence 311, App
Sequence 1053, Ap
Sequence 11919, A
Sequence 11842, A
Sequence 18842, A
Sequence 17721, A
Sequence 3903, Ap
Sequence 3911, Ap
Sequence 3181, Ap
Sequence 3181, Ap
Sequence 2194, Ap
Sequence 2268, Ap
Sequence 2268, Ap
Sequence 2268, Ap
Sequence 2278, Ap
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Sequence 2279, Ap
Sequence 2279, Ap
Sequence 2279, Ap
Sequence 273, Ap
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DB
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0; Mismatches
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OTHER INFORMATION: n can be any nucleotide
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NAME/KEY: variation
LOCATION: 4623
OTHER INFORMATION: n can
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-974-592-3
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Qy Dp	281 281	AATGTGGTTTCTCTTCGGGGGGGGGGGATTGGGGGGGGGG
Qy Db	2341	TAGGGCCCTTTCACTTTCTACTTTTCATTTGTTCTTCGAATTTTTATAAGTAT 2400
Qy	2401	GTATTACTTTTGTAATCAGAATTTTTAGAAAGTATTTTGCTGATTTAAAGGCTTAGGCAT 2460
Oy Dp	2461	GTTCAAACGCCTGCAAAACTACTATCACTCAGCTTTAGTTTTTCTAATCCAAGAAGGCA 2520
oy O	2521	GGGCAGTTAACCTTTTTGGTGCCAATGTGAAATGTAAATGATTTTATGTTTTTCCTGCTT 2580
Qy	2581	4 4
Qy	2641	TITCAAAATAAGTATTICIGAITITGTAAAAIGAAATATAAAATATGTCICAGATCTICC 2700
Qy	2701	CATCCTTAATCCTTGCTAGTTTAAGCCTGCCTAAGTCACTTT 276
Qy Db	2761	ACTAAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTAGGTAAAAGT 2820
Qy	2821	AGAAGCATGTTGTACACTGCTTGTAGTTATAGTGACAGCTTTCCATGTTGAGATTCTCA 2880
Qy	2881	TATCATCTTGTATCTTAAAGTTTCATGTGAGTTTTTACCGTTAGGATGATTAAGATGTAT 2940
QY	2941	
Qy	3001	GTAGATACTICTGAAATAAATGTICTCTCAAGATCCTTAAAACCTCTTGGAAATTATAAA 3060
Qy	3061	aatattggcaagaaagaatagttgtttaaatatttttaaaaaacacttgaatag 3120
Oy Dp	3121	AATCAGTAGGGTATAAACTAGAAGTTTAAAAATGCCTCATAGAACGTCCAGGGTTTACAT 3180
Qy	3181	Tacaagattctcacaacaaacccattgtagaggtgagtaaggcatgttactacagaggaa 3240
Oy Db	3241	agtttgagagtaaaactgtaaaaattatattttgttgtactttctaagagaagagta 3300
Qy Db	3301	TIGITANGITCTCCTAACTICTGITGALTACTACTTTAAGTGAYATTCATTTAAAACAIT 3360

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3361 G	3421	421	18	481	3541 2	541		601	661	3661 G	3721 A	721	3781 A	1 5	841	100	901									4201 A	4201 A	4261 A	4321 G	4321 G	4381 C	4441 A
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LICANT: Human Genome Sciences, Inc., et al.
LICANT: Human Genome Sciences, Inc., et al.
LECANT: Human Genome Sciences, Inc., et al.
LECANT: Nucleic Acids, Proteins, and Antibodies
REFERENCE: PCO02PCT
RETRIENCE: PCO02PCT
RETRIENCE: PCO12PCT
RETRIENCE: PCO12PCT
RETRIENCE: PCO12PCT
RETRIENCE: PCO12PCT
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RETRIENCE: S001-01-14
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4143 4383 4443 3603 1260 3663 3783 3963 3423 ACCACGCCCGGCTAAAACATTGCAAATTTAAATGAGAGTTTTAAAAATTAAATAATGACT 1380 GCCCTGTTTCTGTTTTAGTATGTAAATCCTCAGTTCTTCACCTTTGCACTGTCTGCCACT 1440 GCATITICICIGICITICAACTATAAAAGCACCGGAICTITICCAICTAAITCCGCAAAA 1920 4444 TATCTTTATTTGTAATAATTTAGTCTGCTGATCAAAAGCATTGTCTTAATTTTTGAGAAC 4503 CTTGTATGTTTAGAGTTAAGCAAGACTTTTTTTTTTCTTCCTCTCCATGAGTTGTAAATTTA CTTGTATGTTTAGAGTTAAGCAAGACTTTTTTTTTTCTTCCTCCTCCATGAGTTGTGAAATTTA GCATTGTCTGTGTTGAACTATAAAAAGCACGGATCTTTTCCATCTAATTCCGCAAAA ACCACGCCGGCTAAAACATTGCAAATTTAAATGAGAGTTTTAAAAATTAAATGACT GCCTGTTTCTGTTTTAGTATGTAAATCCTCAGTTCTTCACCTTTGCACTGTCTGCCACT TAGTTTGGTTATATATAGTCATTAACTTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTA **AAGTTTTCTACAAGGGGAGAAAAGTGTTAAAAATTTTTAAAATATGTTTTCCAGGACACTT** CACTICCAAGICAGGIAGGIAGITCAAICIAGIIGTIAGCCAAGGACICAAGGACIGAAI TGTTTTAACATAAGGCTTTTTCCTGTTCTGGGAGCCGCACTTCATTAAAATTCTTCTAAAA ATGCACAACGCTGATGTGGCTAACAAGTTTATTTAAGAATTGTTTAGAAATGCTGTTGC ATTGATCATTTGCAAAGTCAAAACTATAGCCATATCCAAATCTTTTCCCCCTCCCAAGAG TTCTCAGTGTCTACATGTAGACTATTCCTTTTCTGTATAAAGTTCACTCTAGGATTTCAA GTCACCACTTATTTTACATTTTAGTCATGCAAAGATTCAAGTAGTTTTGCAATAAGTACT GAGTGCAGTGGAGTGATCTCTGCTCACTGCAACCTCCGCCTTCTGGGGTTCAAGCGATTCT CGTGCCTCAGCTTCCTGAGTAGCTGGAATTACAGGCAGGTGCCACCATGCCCGACTAATT TITITITITATITITAGTAGAGGGGTTTCACCATGTTGGCCAGGCTGGTATCAAACTCC 1381 1501 1561 1621 1861 2041 1021 1081 3484 1141 1201 3604 1261 3664 1321 3724 3784 3844 3904 3964 4024 1681 4084 1741 4144 1801 4204 4264 1921 4324 1981 4384 3364 3424 3544 셤 g g Q d Q Ω Ω 셤 οy ద δy g δ Q ŏ g δ g ολ g οy Db QY g οy QQ Ω g δý g ò d QΥ Qγ Q 9

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GENERAL INFORMATION:
TILE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PC002C1
CURRENT FILING DATE: 2002-02-22
CURRENT FILING DATE: 2002-02-22
FILO Application removed - See File Wrapper or NUMBER OF SEQ ID NOS: 5116
SOFTWARE: Patentin Ver. 2.0
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3364 AATTTATTTATTTATTTATTTTGAGATGGAGTCTTGCTTG	DD 1201 TITITIATITIAGE GAGGGGGTTCACCATGTGGCCAGGCTGGTATCAACTCC 1260		1501 AAGTTTCTACAAGGGAGAAAAGTGTTAAAATTTTAAAATTTTCCAGGACACTT 1560 09	10	4204 GCATTGTCTGTTTGAACTATAAAAGCACCGGATCTTTCCATCTAATTCCGCAAAA 1861 GCATTGTCTGTTTGAACTATAAAAAGCACCGGATCTTTTCCATCTAATTCCGCAAAA 1861 GCATTGTCTGTTTGAACTATAAAAAAGCACGGATCTTTTCCATCTCAATTCCGCAAAA 4264 ATTGATCATTTGCAAACTATAAAAACAATAGCCATTCCAACTTTCCCTCCC

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Pred. No. 0;
0; Mismatches
                              Query Match 43.5%; Sco
Best Local Similarity 100.0%; Pr
Matches 2328; Conservative 0;
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     ; TYPE: DNA
; ORGANISM: HOMO
US-09-672-717-231
LENGTH: 3000
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TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
FILE REFERENCE: 4-31612 A
CURRENT APPLICATION NUMBER: 05/09/964,899
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/236,893
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 53
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 38
LENGTH: 2404
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7; Conservative
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ORGANISM: Homo Sapien
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Matches 2317;
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; NAME/KEY: CDS
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PCT-US00-00583-1
                                                                                    Similarity
         TYPE: DNA ORGANISM: HOMO
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GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Cowsert
APPLICANT: Lex M. Cowsert
FILE OF INVENTION: ANTISENSE MODULATION OF X-L
FILE REFERENCE: RTSP-0048
CURRENT FILING DATE: 2000-01-10
EARLIER APPLICATION NUMBER: US 09/392,580
EARLIER APPLICATION NUMBER: US 09/392,580
BRILER FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 47
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CONGANISM: Homo sapiens
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APPLICANT: PTC Therapeutics, Inc.
TITLE OF INVENTION: METHODS FOR IDENTIFYING SMALL MOLECULES THAT BIND SPECIFIC 1TILE OF INVENTION: STRUCTURAL MOTIFS
FILLE REFERENCE: 10589-007-228
CURRENT APPLICATION NUMBER: PCT/US02/11757
CURRENT APPLICATION NUMBER: 60/282,965
PRIOR APPLICATION NUMBER: 60/282,965
PRIOR FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VERSION 3.0
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches
                                                                                                                                                      PCT-US02-11757-25; Sequence 25, Application PC/TUS0211757; GENERAL INFORMATION:
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601 TACTACY 661 TGGGAAC 721 TTTTTG 721 GTTTTG 721 GTTTG 721 GTTTG 722 GTTTTG 723 GTTTTG 723 GTTTTG 724 GTTTG 725 GTTTG 726 GTTTG 726 GTTTG 727

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Sequence 15, Application PC/TUS0211758
GENERAL INFORMATION:
SEQUENCE 15, Application PC/TUS0211758
GENERAL INFORMATION:
APPLICANT: PTC Therapeutics, Inc.
TITLE OF INVENTION: METHODS FOR IDENTIFYING SMALL MOLECULES THAT BIND SPECIFIC RNA TITLE OF INVENTION: STRUCTURAL MOTIFS
FILE REFERENCE: 10589-108-128
CURRENT FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: 60/282,966
PRIOR FILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATCHIL VERSION 3.0
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                                                    TCTTTTCAGATAGGCTTAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTA 1920
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100.0%; Pred. No. 0;
Live 0; Mismatches
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Matches 2040; Conservative
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; ORGANISM: Homo sapiens
PCT-US02-11758-25
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PCT-US02-11758-25
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GENERAL INFORMATION:
APPLICANT: Rorneluk, Robert G.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF EQUENCES: 42
CORRESPONDENCE ADDRESS;
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/576,956
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APPLICATION NUMBER: US 08/511,485
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CLASSIFICATION: 435
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MOLECULE TYPE: DNA (genomic)
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2540 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
FILING DATE: 04-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
                                                                                                                                                                     Query Match 38.0
Best Local Similarity 100.
Matches 2040; Conservative
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Oy 1861 TCTTTCAGATAGGCTTAACAATGGAGCTTCTGTATATAATGTGGAGATTAGAGTTA 1920 Db 1861 TCTTTCAGATAGGTTAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTA 1920 Oy 1921 ATCTCCCCAATCACATATTTTTTGTGTGAAAAAGGAATAAATTGTTCCATGCTGGTG 1980 Db 1921 ATCTCCCCCAATCACATATTTGTTTTGTGTGAAAAAGGAATAAATTGTTCCATGCTGTGT 1980 Oy 1981 AGAGATGTTTTAGAGGTTGGTTGTTTTAGGATTCTTTTGTCCATGCTCCATTTTT 2040	1981 GAAAGATAGAGATTGTTTTAGAGGTTGGTTGTGTGTTTTAGGATTCTGTCCATT 2041 T 2041	b 2041 T 2041 ESULT 10 Sequence 3, Application US/08576 GENERAL INFORMATION:	APPLICANT: Korneluk, Robert G. APPLICANT: Mackenzle, Alexander E. APPLICANT: Baird, Stephen APPLICANT: Liston, Peter TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,	NUMBER OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRES ADDRESSEE: Clark A	STREET: CITY: BC STATE: A COUNTRY: 715.	COMPUTER MEDIUM COMPUT	5		ATTORNEY AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30,1	TELECOMMUNICATION INFORMATION: TELEPHONE: 617-428-0200 TELEFAX: 617-428-7045	INFO . SE	STRANDI TOPOLOC MOLECULE	obs 5 ch 1 Similarity 100.0%; Score 1990; DB 9; Length 2540; 1 Similarity 100.0%; Pred. No. 0; 70.00. Conservative 0.	GAAAAGGTGGACAAGTCCTATTTCAAGAGAAGATGACTTTTAACAGTTTTGAAGGATCT 60	1 GAMARGGIGGACARGICCIAIIIICAAGAGAAGAIGACIIIIIAACAGIIIIIGAAGGGAICI

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                   AAGAAAATAATGGAGGAAAAATTCAGATATCTGGGAGCAACTATAAATCACTTGAGGTT
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GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
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TITLE OF INVENTION: PROBES, AND DETECTION MET FILE REFERENCE: 07891/003002

CURRENT APPLICATION NUMBER: US/09/011,356

CURRENT FILING DATE: 1996-09-14

EARLIER FILING DATE: 1996-08-05

EARLIER FILING DATE: 1996-08-05

EARLIER FILING DATE: 1996-12-22

EARLIER FILING DATE: 1996-08-05

EARLIER PELICATION NUMBER: 08/51,485

EARLIER PILING DATE: 1995-08-04

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FASTSEQ for Windows Version 3.0
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LENGTH: 2540
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Matches 2040;
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Oy Dp	721	GTTTGGGCCGGAATCTTAATATTCGAAGTGAATCTGATGCTGTGAGTTCTGATAGGAAT 780
Oy Db	781	CCAAATTCAACAAATCTTCCAAGAAATCCATCCATGGCAGATTATGAAGCAGGATC 84
Qy Dp	841	TTTACTTTTGGGACATGGATATACTCAGTTAACAAGGAGCAGCTTGCAAGAGCTGGATTT 900
Oy Dp	901	TATGCTTTAGGTGAAGGTGATAAAGTGCTTTCACTGTGGAGGGGGTAACTGAT 960
Qy Dp	961	TGGAAGCCCAGTGAAGACCCTTGGGAACAACATGCTAAATGGTATCCAGGGTGCAAATAT 1020
Qy Db	1021	CTGTTAGAACAGAAGGGACAAGAATATATAAACAATATTCATTTAACTCATTCACTTGAG 1080
Oy Op	1081	GAGTGTCTGGTAAGAACTACTGAGAAAACACCATCACTAACTA
oy Ob	1141	ATCTTCCAAAATCCTATGGTACAAGAAGCTATACGAAFGGGGTTCAGTTTCAAGGACATT 1200
Qy	1201	aagaaaataatggaggaaaaaattcagatatctggagcaactataaatcacttgaggtt 1260
Qy Db	1261 1261	CTGGTTGCAGATCTAGTGAATGGTCAGAAAGACAGTATGCAAGATGAGTCAAGTCAGACT 1320
Qy Db	1321	TCATTACAGAAAGAGATTAGTACTGAAGAGCAGCTAAGGCGCCTGCAAGAGGAGAGCTT 1380
Qy	1381	TGCAAAATCTGTATGGATAGAATTATGCTATCGTTTTGTTCCTTGTGGACATCTAGTC 1440
Qy Db	1441	ACTIGIAAACAANGTGCTGAAGCAGTTGACAAGTGTCCCATGTGCTACACAGTCATTACT 1500
Qy Dp	1501	TICAAGCAAAAAITITIAIGICITAAICIAAAGICIAIAGIAGGCAIGITAAGITGITCI 1560
Qy Db	1561	TATTACCCTGATTGAATGTGATGTGAACTGACTTTAAGTAATCAGGATTGAATTCCAT 1620
Oy Dp	1621	TAGCATTTGCTACCAAGTAGGAAAAAATGTACATGGCAGTGTTTTAGTTGGTGCCATATA 1680
Qy Dp	1681	AICTITGAAITICITGAITITICAGGGTATTAGCIGTAITATCCAITITITITACICITA 1740
Oy Db	1741	TITAATIGAAACCATAGACTAAGAATAAGAACATCATACTATAACTGAACAAATGIGT 1800

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TCTTTTCAGATAGGCTTAACAAATGGAGCTTTCTGTATATAAATGTGGAGATTAGAGTTA 1920
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GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Bard, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003002
CURRENT APPLICATION NUMBER: US/09/011,356A
CURRENT APPLICATION NUMBER: 08/71,1896/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/51,485
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
SEARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-04
SEARLIER FILING DATE: 1995-08-04
SEARLIER FILING DATE: 1995-08-04
SOFTWARE: FELING DATE: 1995-08-04
SOFTWARE: FastSEQ for Windows Version 4.0
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38.0%; Score 1990; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches
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: LOCATION: (2540)...(2540)

: OTHER INFORMATION: N may be any nucleotide

US-09-011-356-3
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Sequence 900, Application US/09023655

GENERAL INPORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, IN
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
CITY: PALO ALTO
COUNTRY: USA
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COUNTRY: USA
THE COUNTRY: USA
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for W
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2040; Conservative 0; Mismatches
                                                                                     0S
      US/09/023,655
                                                                                   REFERENCE/DOCKET NUMBER: PA-0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                         TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 900:
SEQUENCE CHARACTERISTICS:
LENGTH: 2540 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                           37,071
                                                            ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,
DATA:
     APPLICATION NUMBER: US
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
              HEREWITH
CURRENT APPLICATION
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                                                                                                                                                                        ; LIBRARY: GENBANK
; CLONE: 91184319
US-09-023-655-900
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APPLICANT: Chenchik, Alex
TITLE OF INVENTION: Nucleic Acid Arrays
TITLE REPERENCE: CLON-006
CURRENT APPLICATION NUMBER: US/09/053,375B
CURRENT FILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 1543
SEQ ID NO 2190
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APPLICANT: Korneluk, Robert G.
APPLICANT: MacKenzle, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Baird, Stephen
APPLICANT: Baird, PERPEN
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMER
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REPERENCE: 07891/00304
CURRENT APPLICATION NUMBER: US/09/201,932
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 08/011,356
EARLIER FILING DATE: 1996-08-05
EARLIER FILING DATE: 1995-08-05
EARLIER FILING DATE: 1995-08-05
EARLIER PILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSEQ for Windows Version 3.0
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OTHER INFORMATION: N may be any nucleotide
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APPLICANT: Korneluk, Robert G.
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/USO6_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 29306, A Sequence 28292, A Sequence 26027, A Sequence 20475, A Sequence 20475, A Sequence 1470, A P Sequence 1101, A P Sequence 1101, A P Sequence 1101, A P Sequence 1, Appli Sequence 1, Appli Sequence 27025, A Sequence 5, Appli Sequence 6, Appli Description US-09-513-999C-29306 US-09-513-999C-28292 US-09-513-999C-262944 US-09-513-999C-26294 US-09-513-999C-26277 US-10-271-416-9 US-09-513-999C-20475 US-10-240-425-1470 US-09-513-999C-18190 US-09-513-999C-18190 US-10-240-425-1101 US-10-240-425-1102 US-09-513-999C-22123 US-09-513-999C-22123 US-09-513-999C-22123 US-09-513-999C-22123 US-09-513-999C-22123 US-10-240-851-6 Query Match Length DB 2.9 190 1.6 237 1.5 276820 1.5 276820 1.3 271 1.3 133760 1.3 334205 1.3 334205 1.3 334205 1.3 334205 1.3 334205 1.3 334205 1.3 334205 1.3 334205 1.3 334205 1.3 334205 1.3 334205 1.3 334205 1.3 342 Result No.

Sequence 19193, A Sequence 6, Appli Sequence 27657, A Sequence 21657, A Sequence 21453, A Sequence 2355, A Sequence 23555, A

Sequence 1450, Ap

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27 67 11.1 11.1 11.1 11.1 11.1 11.1 11.1 11		RESULT 1 US-09-513-999C-29306 Sequence 29306, Application US/0951: GENERAL INFORMATION: APPLICANT: Dumas Milne Edwards, J.I. APPLICANT: Duclert, A. TITLE OF INVENTION: Expressed Seque TITLE OF INVENTION: Expressed Seque CURRENT FILING DATE: 2000-02-24 CURRENT PRILIGATION NUMBER: US/09/; CURRENT FILING DATE: 1999-02-26 NUMBER OF SEQ ID NOS: 36681 SOFTWARE: PATCHT, PM SEQ ID NO 29306 LENGTH: 315 LENGTH: 315 LENGTH: 315 US-09-513-999C-29306	Similarity 4; Conservat	AATTCTTCT 	GTTGTGAAA GTTGTGAAA	GAAATGCTG	TGGAGACTI TGGAGACTI	TAATTCCGC	CTTTTCCCCCTCCC
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US-10-271-416-9/c
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                                              Sequence 28292, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Duclart, A.
APPLICANT: Diclard, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 1090-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 28292
LENGTH: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2121 ATACTATCGAGCCAACATGTACTGACATGGAAAGATGTCAAAGATATGTTAAGTGTAAAA 2180
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APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR PPLICATION NUMBER: 05.60/122,487
PRIOR FILING DATE: 1999-02-26
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100.0%; Pred. No. 1.7e-21;
iive 0; Mismatches 0;
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US-09-513-999C-25994/c
; Sequence 25994, Application US/09513999C
; GENERAL INFORMATION:
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US-09-513-999C-28292
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Best Local Similarity 100.0
Matches 151; Conservative
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SOFTWARE: Patent.pm
SEQ ID NO 25994
LENGTH: 237
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tes 85; Conservative
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US-09-513-999C-25994
                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Homo sapiens
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                                   US-09-513-999C-28292
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APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Unclert, A.
APPLICANT: Unclert, A.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
SOFTWARE: PALENT.PM
SEQ ID NO 26027
LENGTH: 237
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APPLICANT: Workstown Tim
APPLICANT: Work Edwerph Paul
APPLICANT: Van Berdewerph, Paul
APPLICANT: Use Berdewerph, Paul
APPLICANT: Dupuis, Josee
APPLICANT: Del Mastro, Richard G.
APPLICANT: Allen, Kristina
APPLICANT: Allen, Kristina
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
FILE REFERENCE: 2976-4045
CURRENT APPLICATION NUMBER: US/10/271,416
CURRENT FILING DATE: 2002-10-11
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 9
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 2.2e-19;
Matches 79; Conservative 0; Mismatches 0;
US-09-513-999C-26027/c
; Sequence 26027, Application US/09513999C
; GENERAL INFORMATION:
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US-09-513-999C-26027
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ORGANISM: Homo sapiens
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LOCATION: 119
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ORGANISM: Homo sapien
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SEQ ID NO 396
LENGTH: 5574
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US-09-513-999C-20475/c
US-09-513-999C-20475, Application US/09513999C
Sequence 20475, Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.052.REG
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GENERAL INFORMATION:
APPLICANT: Williams, Amanda
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Scherf, Uwe
APPLICANT: Vockley, Joseph G.
APPLICANT: Vockley, Joseph G.
APPLICANT: Wetzel, John C.
APPLICANT
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                                                                                                                                                                                                                      1.5%; Score 79; DB 6; Length 276820;
100.0%; Pred. No. 4e-20;
Live 0; Mismatches 0; Indels 0
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NAME/KEY: conflict

: LOCATION: (167043)...(167043)

: OTHER INFORMATION: Y=C or T

US-10-271-416-9
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US-09-513-999C-20475
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Best Local Similarity 100.0
Matches 79; Conservative
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SOFTWARE: Patent.pm
SEQ ID NO 20475
LENGTH: 271
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APPLICANT: Boland, Joseph F.
APPLICANT: Boland, Joseph F.
APPLICANT: Lord, Reginald V.
APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Wetzel, Jon C.
APPLICANT: Wetzel, Jon C.
APPLICANT: Wockley, Joseph G.
APPLICANT: Wockley, Joseph G.
APPLICANT: Wockley, Joseph G.
APPLICANT: Wockley, Joseph G.
APPLICANT: Workley, Joseph G.
APPLICANT: POLOGNEN: 14921-5026
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2001-03-28
PRIOR FILING DATE: 2001-03-28
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: Patentin Ver. 2.1
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US-10-240-425-396
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100.0%; Pred. No. 5.8e-19;
iive 0; Mismatches 0;
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; OTHER INFORMATION: Genbank Accession No. U89337
US-10-240-425-1470
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US-09-513-999C-18190
; Sequence 18190, Application US/09513999C
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
                             60/193,446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 396, Application US/10240425 GENERAL INFORMATION:
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60,
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: PALENTIN VET: 2.1
SEQ ID NO 1470
LENGTH: 100267
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Best Local Similarity 100.0
Matches 76; Conservative
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ORGANISM: Homo sapiens
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Db 120084 AAAATTAGCCGGGCGTGGTGGCGGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCA 120143
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APPLICANT: Lord, Reginald V.
APPLICANT: Alvarez, Chris
APPLICANT: Wetzel, Jon C.
APPLICANT: Scherf, Uwe
APPLICANT: Vockley, Joseph G.
TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue PILE REFERENCE: 44921-5202
CURRENT APPLICATION NUMBER: US/10/240,425
CURRENT FILING DATE: 2002-09-30
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APPLICANT: Van Eerdewegh, Paul
APPLICANT: Van Eerdewegh, Paul
APPLICANT: Del Mastro, Richard G.
APPLICANT: Allen, Kristina
TITLE OF INVENTION: NUCLEOTIDE AND AMINO ACID SEQUENCES
TITLE OF INVENTION: REPERFICE: 2976-4045
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7.7.1e-16;
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1.3%; Score 69; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 1.6e-16;
Matches 69; Conservative 0; Mismatches 0;
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US-10-240-425-1101
                                                                                                                           Query Match 1.3%; Score 69; DB Best Local Similarity 100.0%; Pred. No. 7.1 Matches 69; Conservative 0; Mismatches
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PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/193,446
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 1588
SOFTWARE: PAtentin Ver. 2.1
SEQ ID NO 1101
LENGTH: 133760
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GENERAL INFORMATION:
APPLICANT: Keith, Tim
                                                       ; OTHER INFORMATION: s=g or c US-09-513-999C-32057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Williams, Amanda APPLICANT: Boland, Joseph
            NAME/KEY: misc_feature
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ORGANISM: Homo sapiens
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APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.052.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SSC ID NO 18190
LENGTH: 212
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| Sequence 32057, Application US/09513999C
| GENERAL INFORMATION:
| APPLICANT: Dumas Milne Edwards, J.B.
| APPLICANT: Duclert, A.
| APPLICANT: Duclert, A.
| APPLICANT: Duclert, A.
| APPLICANT: Diversion of J.Y.
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
| FILE REPRENCE: 59.US2.REG
| CURRENT APPLICATION NUMBER: US/09/513,999C
| CURRENT FILING DATE: 2000-02-24
| PRIOR FILING DATE: 2000-02-24
| PRIOR FILING DATE: 1999-02-26
| NUMBER OF SEQ ID NOS: 36681
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Best Local Similarity 100.0%; Pred. No. 7.2e-16;
Matches 69; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: k=g or t
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OTHER INFORMATION: y=c or t
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; LOCATION: 212
; OTHER INFORMATION: r=a or g
US-09-513-999C-18190
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LOCATION: 200
OTHER INFORMATION: w-a or
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 184
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OTHER INFORMATION: m-a
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ORGANISM: Homo sapiens
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LENGTH: 231
                                                                                                                                                                                                                                                                                         TYPE: DNA
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Bougueleret, Lydie

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US - 10-14/4-20-110

Sequence 1102, Application US/10240425

GENERAL INFORMATION:

APPLICANT: Williams, Amanda

APPLICANT: Boland, Joseph F.

APPLICANT: Lord, Reginald V.

APPLICANT: Alvarez, Chris

APPLICANT: Alvarez, Chris

APPLICANT: Alvarez, Chris

APPLICANT: Scherf, Uwe

APPLICANT: Workley, Joseph G.

TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue

FILE REFERENCE: 4091-5026

CURRENT APPLICATION NUMBER: US/10/240,425

CURRENT APPLICATION NUMBER: US/00-09-30

PRIOR FILING DATE: 2001-03-28

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 1588

SOFTWARE PATENTIN VET. 2.1

SEQ ID NO 1102

LENGTH: 134292
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                                                                                                                                                                                                                                                                           Length 304905;
                                                                                                                                                                                                                                                                    Query Match 1.3%; Score 69; DB 6; Length 304 Best Local Similarity 100.0%; Pred. No. 1.3e-16; Matches 69; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AL031983
US-10-240-425-1102
CURRENT APPLICATION NUMBER: US/10/271,416
CURRENT FILING DATE: 2002-10-11
PRIOR PILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 9
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 304905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-539-333D-1
; GENERAL INFORMATION:
APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapien
US-10-271-416-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 25159 GGAGAATGG 25167
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| Db 113378 TAAAAA 113384
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US-10-240-425-1102
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APPLICANT: BIALIN, BETNARD

APPLICANT: BIALIN, BETNARD

APPLICANT: BIALIN, BETNARD

APPLICANT: ESSIOUX, LAURENT

TITLE OF INVENTION: SCHIZOPHERNIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS

FILE REFERENCE: GENSET: 047AUS

CURRENT APPLICATION NUMBER: US 60/126,903

PRIOR PELING DATE: 1999-03-30

PRIOR PELING DATE: 1999-04-30

PRIOR PELING DATE: 1999-04-30

PRIOR PELING DATE: 1999-07-39

PRIOR PELING DATE: 1999-07-39

PRIOR PELING DATE: 1999-07-44

PRIOR PELING DATE: 1999-07-44

PRIOR PELING DATE: 1999-07-29

PRIOR PELING DATE: 1999-07-29

PRIOR APPLICATION NUMBER: US 60/146,453

PRIOR PELING DATE: 1999-07-29

PRIOR PELING DATE: 1999-10-28

PRIOR PELING DATE: 1999-10-28

PRIOR PELING DATE: 1999-10-12

PRIOR PELING DATE: 1999-10-12
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OTHER INFORMATION: polymorphic base A or C
FEATURE:
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OTHER INFORMATION: polymorphic base GFEATURE:
NAME/KY: allele
LOCATION: 111978
OTHER INFORMATION: polymorphic base A
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LOCATION: 112468
OTHER INFORMATION: polymorphic base G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 118972
OTHER INFORMATION: polymorphic base C
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OTHER INFORMATION: polymorphic base C
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OTHER INFORMATION: polymorphic base A
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OTHER INFORMATION: polymorphic base A
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OTHER INFORMATION: polymorphic base
FEATURE:
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OTHER INFORMATION: deletion ACTT
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FEATURE:
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NAME/KEY: allele
LOCATION: 119160.
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NAME/KEY: allele
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LOCATION: 126105 OTHER INFORMATION:	FEATURE: NAME/KEY: allele LOCATION: 129789 OTHER INFORMATION:	RE: KEY: allele ION: 130777	OTHER INFORMATION: FEATURE:	: allele : 136942 FORMATION:	FEATURE: NAME/KEY: allele	9	NAME/KEY: allele LOCATION: 146668	OTHER INFORMATION: FEATURE: NAME/KEY: allele	LOCATION: 147281 OTHER INFORMATION:	FEATURE: NAME/KEY: allele	LOCATION: 147505 OTHER INFORMATION:	FEATURE: NAME/KEY: allele	LOCATION: 148183 OTHER INFORMATION:	FEATURE:	LOCATION: 148372 OTHER INFORMATION:	FEATURE:	LOCATION: 149012	OTHER INFORMATION: FEATURE:	NAME/KEY: allele LOCATION: 149113	OTHER INFORMATION: FEATURE:	NAME/KEY: allele	OTHER INFORMATION:	NAME/KEY: allele	OTHER INFORMATION:	FEATURE: NAME/KEY: allele	LOCATION: 151769 OTHER INFORMATION:	FEATURE: NAME/KEY: allele	LOCATION: 151847 OTHER INFORMATION:	FEATURE:	LOCATION: 152691 OTHER INFORMATION:	FEATURE:	LOCATION: 152766 OTHER INFORMATION:	FEATURE:	LOCATION: 153046
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Db 276617 AAAATTAGCCGGGCGTGGTGGCGGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGC 276676 5062 AAAATTAGCCGGGCGTGGTGGCGGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCA 5121 0; Gaps Ouery Match 1.3%; Score 67; DB 5; Length 319608; Best Local Similarity 100.0%; Pred. No. 6.4e-16; Matches 67; Conservative 0; Mismatches 0; Indels 0 LOCATION: 157238
OTHER INFORMATION: polymorphic base A or C FEATURE:
NAME/KEY: allele
LOCATION: 157897
OTHER INFORMATION: polymorphic base A or G FEATURE:
NAME/KEY: allele
LOCATION: 158172
OCHER INFORMATION: polymorphic base A or G FEATURE:
COCATION: 158172
OTHER INFORMATION: polymorphic base A or G FEATURE: COTTENT INFORMATION: POLYMOLPHIC DASE A OLD STREATURE:
NAME/KEY: allele
LOCATION: 154879
OTHER INFORMATION: polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 155802
OTHER INFORMATION: polymorphic base G or T
FEATURE:
NAME/KEY: allele
LOCATION: 155802
OTHER INFORMATION: polymorphic base C or T
FEATURE:
NAME/KEY: allele
LOCATION: 156448
OTHER INFORMATION: polymorphic base A or G
FEATURE:
NAME/KEY: allele
LOCATION: 156448
OTHER INFORMATION: polymorphic base A or G
FEATURE:
NAME/KEY: allele OTHER INFORMATION: polymorphic base C or T FEATURE:
NAME/KEY: allele
LOCATION: 153123
OTHER INFORMATION: polymorphic base A or G FEATURE:
NAME/KEY: allele
LOCATION: 153925
OTHER INFORMATION: polymorphic base C or T FEATURE:
NAME/KEX: allele or or or LOCATION: 153977
OTHER INFORMATION: polymorphic base G or PERTURE:
NAME/KEY: allele
LOCATION: 154502
OTHER INFORMATION: polymorphic base C or PERTURE:
NAME/KEY: allele
LOCATION: 154677
OTHER INFORMATION: polymorphic base A or OTHER INFORMATION: polymorphic base A or OTHER INFORMATION: RESULT 15
US-09-539-33D-1
Sequence 1, Application US/0953933D
Sequence 1, Application US/0953933D
SEQUENCE INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Chumakov, Ilya
APPLICANT: Bougueleret, Lydie
APPLICANT: Bihain, Bernard Qy 5122 GGAGAAT 5128 δ

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NAME/KEY: exon
LOCATION: 231272..231412
OTHER INFORMATION: exon Obis complement 934872 gene
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LOCATION: 237406..237428
OTHER INFORMATION: exon Nbis complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 215819..215975
OTHER INFORMATION: exon Rbis complement 934872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 216661..216952
OTHER INFORMATION: exon Qbis complement 934872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: 213818..215818
OTHER INFORMATION: 3'regulatory region g34872 gene
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LOCATION: 217027..217061
OTHER INFORMATION: exon Q1 complement 934872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 239719..239807
OTHER INFORMATION: exon N2 complement g34872 gene
FEAPURE:
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LOCATION: 231787..231880
OTHER INFORMATION: exon '02 complement 934872 gene
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LOCATION: 231870..231879
OTHER INFORMATION: exon Ol complement 934872 gene
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LOCATION: 215819..215941
OTHER INFORMATION: exon R complement g34872 gene
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LOCATION: 216661..217061
OTHER INFORMATION: exon Q complement g34872 gene
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LOCATION: 234174..234321
OTHER INFORMATION: exon O complement g34872 gene
FEAPIRE:
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LOCATION: 229647..229742
OTHER INFORMATION: exon X complement g34872 gene
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                                                       NAME/KEY: exon
LOCATION: 201188..201234
OTHER INFORMATION: exon S 935030 gene
                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 214676..214793
OTHER INFORMATION: exon T 935030 gene
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LOCATION: 216836..216915
OTHER INFORMATION: exon V 935030 gene
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LOCATION: 215702..215746
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230408..230721
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LOCATION:
### APPLICANT: ESSIOUX, LAUTENT
### TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
### CURRENY APPLICATION NUMBER: US/09/539,333D
### CURRENT FILING DATE: 2000-03-30
### PRIOR PELICATION NUMBER: US 60/136,903
### PRIOR PLICATION NUMBER: US 60/131,971
### PRIOR PLICATION NUMBER: US 60/131,971
### PRIOR PLICATION NUMBER: US 60/132,065
### PRIOR PLICATION NUMBER: US 60/132,065
### PRIOR FILING DATE: 1999-04-30
### PRIOR FILING DATE: 1999-04-30
### PRIOR FILING DATE: 1999-07-14
### PRIOR FILING DATE: 1999-07-29
### PRIOR FILING DATE: 1999-10-28
### PRIOR FILING DATE: 1999-10-12
### PRIOR FILING DATE: PATENT PATE: PATENT PATEN
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NAME/KEY: misc_feature
LOCATION: 31.1107
OTHER INFORMATION: 5'regulatory region g35018 gene
FEATURE:
NAME/KEY: exon
LOCATION: 1108..1289
OTHER INFORMATION: exon A g35018 gene
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LOCATION: 65854..67854
OTHER INFORMATION: 3'regulatory region g35018 gene
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LOCATION: 25593..25740
OTHER INFORMATION: exon C 935018 gene
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LOCATION: 29388..29502
OTHER INFORMATION: exon D 935018 gene
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LOCATION: 14877..14920
OTHER INFORMATION: exon B 935018 gene
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LOCATION: 29967..30282
OTHER INFORWATION: exon E 935018 gene
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LOCATION: 64666..64812
OTHER INFORMATION: exon F 935018 gene
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LOCATION: 65505..65853
OTHER INFORMATION: exon G 935018 gene
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LOCATION: 94124..94964
OTHER INFORMATION: exon 935017
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ORGANISM: Homo sapiens
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LOCATION: 18778..18862
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LENGTH: 319608
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1.3%; Score 67; DB 5; Length 319608;
Best Local Similarity 100.0%; Pred. No. 6.4e-16;
Matches 67; Conservative 0; Mismatches 0; Indels 0
                                                                                                 NAME/KEY: exon
LOCATION: 240528..240569
OTHER INFORMATION: exon M1117 complement g34872 gene
FEATURE:
LOCATION: 240528..240596
OTHER INFORMATION: exon M1090 complement g34872 gene
                                                                                                                                                                                                                                                                                                 NAME/KET: exon
LOCATION: 240528..240617
OTHER INFORMATION: exon M1069 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: exon
LOCATION: 240528..240824
OTHER INFORMATION: exon M862 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: exon
COGATION: 240594
COGATION: 240528..240994
COTHER INFORMATION: exon M692 complement g34872 gene FEATURE:
NAME/KEY: exon
COCATION: 240528..241685
OTHER INFORMATION: exon MI complement g34872 gene FEATURE:
FEATURE:
FEATURE:
FEATURE:
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NAME/KEY: excon
LOCATION: 240528..240644
OTHER INFORMATION: excon MS2 complement g34872 gene
FEATURE:
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LOCATION: 241686..243685
OTHER INFORMATION: 5'regulatory region g34872 gene
FRATURE:
NAME/KEY: misc_feature
LOCATION: 290652..292652
OTHER INFORMATION: 3'regulatory region g34665 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: exon
LOCATION: 240800..240993
OTHER INFORMATION: exon MS1 complement g34872 gene
NAME/KEY: exon
LOCATION: 239719..239853
OTHER INFORMATION: exon N complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY: exon
LOCATION: 292653..292841
OTHER INFORMATION: exon B complement g34665 gene
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Qy 5062 AAAATTAGCCGGCGTGGTGGCGGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCA 5121
Db 276617 AAAATTAGCCGGGCGTGGTGGCGGGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCA 276676

Oy 5122 GGAGAAT 5128

|||||||| |Db 276677 GGAGAAT 276683

Search completed: November 10, 2002, 05:25:04 Job time : 3430 secs

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AW750285 PM0-BT058
BE220552 ht98a01.x
BE380045 601159359
BG423165 AGENCOURT
AA115728 Z186h12.r
AB115728 Z186h12.r
AR395438 601433915
AA997840 oq33£09.s
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AV706807 AV706807
AA295472 EST100639
BQ233403 AGENCOURT
Z41329 HSCZQG052 n
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BI821020 603039619
AI41837 t448812.x
BI09433 602860253
BF754025 CM2-CT500
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AU123207 AU123207
BQ369513 RC3-GN007
AA345330 EST51334
AR807831 MR4 ST009
AW675725 ba53e09.x
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                 BF510268 UI-H-BI4-
BG164322 602341372
AI277821 qm60e01.x
AI299965 qo24all.x
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H64979 yu66a10.s1
BE813985 QV3-BN004
BE815593 PMO-BN016
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rfmail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
POLYA-Yes.
                                                                                AW665401 h190c08.x
BE222433 hv90g11.x
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 757)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                               BG164322
AI227821
AW665401
BE222433
AL6815423
BI823020
BIRD4023
BIRD40285
AL18825
AL18825
AL18825
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AW675725
AI861853
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BQ369513
AA345330
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BE815593
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12852.235 Million cell updates/sec
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                                                                                                             9, 2002, 19:46:46; Search time 6593 Seconds
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                 GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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Gapop 60.0 , Gapext 60.0
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Minimum DB seq Maximum DB seq

Database :

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Searched:

Perfect score:

Run on:

Sequence:

Scoring table:

Location/Qualiflers
1..757

source

FEATURES

BQ007511 UI-H-EDI-BG502660 602549490 BM459898 AGENCOURT AI628066 ty84b02.x AL713196 DKFZp686M BM990097 UI-H-DIO-

BQ007511 BG502660 BM459898 AI628066 AL713196 BM990097

14 13 14 14

757 822 1041 784 529 691

12.3 10.9 10.8 9.0 8.7

641 571 567 551 469 455

Description

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Score

Result Š.

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113 GCTTTCTGTATATATGTGGAGATTAGAGTTAATCTCCCC 73
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TITLE
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KEYWORDS
SOURCE
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//dev_stage="honogrosarcoma call site_2: Not !; NCI_CGAP_ED1 is a normalized cDNA library
//decage containing the following tissue(s): Chondrosarcoma cell
//denon and Soares, Genome Research, 6:791-806, 1996.
//first strand cDNA synthesis was primed with an oligo-dr
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
//decage directionally into pr773-pac vector. The
//district containing allowed the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dr)18 tail. The
//decage contains a library is GCTCAAGGCT.
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                                                                /clone_lib="NCI_CGAP_ED1"
/tissue_type="Chondrosarcoma"
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                                      /clone="IMAGE:5836323"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Inbe"Index:467102"
/clone="Index:467102"
/clone="
BG502660 822 bp mRNA linear EST 27-MAR-2001 602549490F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4657102 5',
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 822)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capaba-riemail.inh.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1449 row: c column: 23
High quality sequence stop: 670.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/note="Organ: uterus; Vector: pcMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned_unidirectionally. Primer: Oligo dT.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
             241 AGGCCATCTGAGACACATGCAGACTATCTTTTGAGAACTGGGCAGGTTGTAGATATATCA 300
                                                                                                                                                          TACACAGGTATTGGTGACCAAGTGCAGTGCTTTTGTTGTGGTGGAAAAACTGAAAATTGG 663
                                                                                                                                                                                                             GAACCTTGTGATCGTGCTGGTCAGAACACAGGCGACACTTTCCTAATTGCTTCTTTGTT 723
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can ifound through the I.M.A.G.E. Consortium/LLNL at:
http://maqe.lnl.gov
Plate: LLAM1215 row: d column: 08
High quality sequence stop: 567.
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                                                   GACACCATATACCCGAGGAACCCTGCCATGTATAGTGAAGAAGCTAGATTAAAGTCCTTT
                                                                AGGCCATCTGAGACACATGCAGACTATCTTTTGAGAACTGGGCAGGTTGTAGATATATAA
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In Dupublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmail: Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 784)
NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                              TTAAAAAACTTTTGCTAATTTTCCAAGTGGTAGTCCTGTTTCAGCATCAACACTGGCACGA 180
AAAACTTGTGTACCTGCAGACATCAATAAGGAAGAAGTTTGTAGAAGAGTTTAATAGA 120
                                                                                                                                                                                                                                                                                                                                              TGCAGATTTATCAACGGCTTTTATCTTGAAAATAGTGCCACGCAGTCTACAAATTCTGGT
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A1628066.1 GI:4664866
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                                                                                            /note="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: NOt I; Site_2: ECO RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hypridization reaction. The diriver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and Fastima Ronald.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL713196 529 bp mRNA linear EST 22-MAR-2002 DKFZp686M1895_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686M1895 5', mRNA sequence.
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                                                                     /clone_lib="NCI_CGAP_Kid11"
/lab_host="DH108"
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                           /clone="IMAGE:2285739"
           Location/Qualifiers
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152 c 10
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                                                                 1 (bases 1 to 529)
Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                               EST (Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B. and
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No s1 sequence available.
This clone (DKFzp686M1895) is available at the RZPD in I
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Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
_Location/Qualifiers
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/clone_lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH108"
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/db_xref="taxon:9606"
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100.0%; Pred. No.
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Unpublished (1999)
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E I (bases 1 to 691)

Noticona to force institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov Mercuende CDNA Library preparation: Dr. Jose Mercuende CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Distribution: Clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="Indace: 1885"
/clone="Indace: 1885"
/clone="Lib="NCI CGAP_DIO"
/tissue_type="Lung Focal Fibrosis"
/dev_stage="Adult"
/lab host="DH10B (Life Technologies)"
/note="Organ: Lung; Vector: pT773-pec (Pharmacia) with a modified polylinker; Site_1: ECOR I; Site_2: Not I; NCI_CGAP_DIO is a cDNA library containing the following tissue(s): A pool of Lung Focal Fibrosis. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dr primer containing a Not I site. Double stranded cDNA was ligated to an ECOR adaptor, digested with Not I, and cloned directionally into PT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the Name of the contains and the Name of the contains and the labrary is
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                                                                        EST 17-JUN-2002
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The following repetitive elements were found in this cDNA
sequence: 11-298, >ALU (matched compliment)
Seq primer: MI3 FORWARD
POLYA-Yes.
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                                                  691 bp mRNA linear EST 17-JUN-
UI-H-DIO-ato-n-20-0-UI.s1 NCL_CGAP_DIO Homo sapiens cDNA clone
IMAGE:5862355 3', mRNA sequence.
BM990097
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Pred. No. 0;
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/db_xref="taxon:9606"
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4744 ATTTGTATTTTGAACTATGAATGGAGACTACCGCCCAGCATTAGTTTCACATGATATAC 4803

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/clone_lib="NIH_MGC_76"
/lab_host="DH10B (T1 phage-resistant)"
/note="Corgan: liver; Vector: pDNR-LIB (Clontech); Site_1:
/for gecgctcggcc); Site_2: Sfil (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG616695 537 bp mRNA linear EST 18-APR-2001
602614908F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4733808 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens Eutrazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Maukaryola; Metazoa; Chordata; Catarrhini; Hominidae; Homo. 1 (bases 1 to 537)
1 (hases 1 to 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5104 ACTCGGGAGGCTGAGGCAGGAGAATGGTGAACCCGGGAGGCAGAGCTTGCAGTGAGCC 5163
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Preparation: CLONETECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Hitp://mage.lln.gov
Plate: LLCM595 row; p column: 01

High quality sequence stop: 537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4984 AGGCAGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACACCGTGAAACCCC 5043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70
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                                                                                                                                                                                                                                                    109 AAATAAAATGGGGCTGGGCTCACTGGTCACCCTGTAATCCCAGCACTTTGGGAGGTG
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/clone="IMAGE:4733808"
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1. .537
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5'-ATTCTAGAGGCCGAGGCGCGATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85 kb (range 1.0 -4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NII_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
I.M.A.G.E. Consortium/Lim. at:
www-blo.llnl.gov/bbrp/image/image.html
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5'-CACGCCCATTATGCCC-3' and 3' adaptor sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 46). NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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UI-H-BI4-api-d-01-0-UI.sl NCI_CGAP_Sub8 Homo sapiens cDNA clone
IMAGE:3087408 3', mRNA sequence.
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                                                                                                                                                                                                                                                                    4169 CTCCAACTICTAATCAAATTTTTGGAGACTTAACAGCATTTGTCTGTGTTTGAACTATAA 4228
                                                                                                                                                                                                                                                                                                                                              4229 AAAGCACCGGATCTTTCCATCTAATTCCGCAAAAATTGATCATTTGCAAAGTCAAAACT 4288
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                                                                                                                                                                                              Length 537;
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100.0%; Pred. No. v.
... 0; Mismatches
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Unpublished (1997)
                                                                                                                                                                                                                                  Conservative
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BF510268/c
LOCUS
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ORIGIN
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Matches
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AUTHORS
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KEYWORDS
SOURCE
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/clone="Inackon:900"
/clone="Inackon:900"
/clone="Inackon:900"
/clone_lb="NoI_Cap_Gub8"
/lab_lost="Dello" NoI_Cap_gub8"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_l: NoI !; Site_2: Eco RI; NoI_CGAP_Sub8
is a subtracted library derived from NoI_CGAP_Sub5
NoI_CGAP_Sub8 library derived from NoI_CGAP_Sub5
NoI_CGAP_Sub8 library had 2.5 million recombinants. A
single-stranded DNA preparation of NoI_CGAP_Sub5 was used
as a tracer in a subtractive hybridization with a driver
comprising; a pool of clones from NoI_CGAP_Sub5 (IMAGE
clone Ids 273283-2737415, 3068040-3069191; 25% of the
driver population), a pool of clones from NOI_CGAP_Sub4
(IMAGE clone Ids 2723592-2729326; 25% of the driver
population), NOI_CGAP_Sub6 (pool AIF-AJU, IMAGE Ids
2728569-2733190; 25% of the driver population), and
NOI_CGAP_Sub7 (IMAGE Ids 3069192-3072238, 308164-3084550
; 25% of the driver population). Subtraction was
performed as previously described [Bonaldo, Lennon &
Soares (1996): Normalization and Subtraction: Two
Approaches To Facilitate Gene Discovery, Genome Research
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100.0%; Pred. No. v.
... 0; Mismatches
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    462
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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TAG_TISSUE=lung
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                                            Location/Qualifiers
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Seq primer: M13 Forward POLYA=Yes.
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Matches 434; Conservative
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BG164322
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                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
Tissue Procurement: Arg.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
Plate: LLAM10232 row: p column: 17
High quality sequence stop: 670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="hypernophroma, cell line"
/lab_host="hypernophroma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Grgan: Ridney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full:length clones and constructed by Life Technologies.
Note: this is a NHH_MGC Library."
                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 943)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
602341372F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4449280 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTTTCCAGGACACTTCACTTCCAAGTCAGGTAGGTAGTTCAATCTAGTTGTTAGCCAA 3946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4247 CATCTAATTCCGCAAAAATTGATCATTTGCAAAGTCAAAACTATAGCCATATCCAAATCT 4306
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4449280"
/clone_lib="NIH_MGC_89"
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                                                     BG164322.1 GI:12671025
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Best Local Similarity 99.7%;
Matches 602; Conservative
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BG164322
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A1277821
A1277821.1 G1:3900089
EST.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (268s 1 to 472)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nh.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2306 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 438.
Location/Qualifiers
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                                          TTTCCCCCCTCCCAAGAGTTCTCAGTGTCTACATGTAGACTATTCCTTTTTCTGTATAAAGT
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/db_xref="taxon:9606"
/clone="IMAGE:1893144"
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AI277821/c
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Length 406

DB 9;

7.8%; Score 406;

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Best Local Similarity
Matches 406; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: WWW-bb.llnL gov/Dbrp/Mage-/image-html
Insert Length: 491 Std Error: 0.00
Seq primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI299965 406 bp mRNA linear EST 01-FEB-1999 qo24a11.x1 NCI_CGAP_Lu5 Homo sapiens CDNA clone IMAGE:1909436 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 406)

NCI-GAAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
1660 AGTGTTTTAGTTGGCAATATAATCTTTGAATTTCTTGATTTTTCAGGGTATTAGCTGTAT 1719
                                                                        1720 TATCCATTTTTTTACTGTTATTTAATTGAAACCATAGACTAAGAATAAGAAGCATCATA 1779
                                                                                                                                               1840 TTAATCATCTGGATTTTTTTTTTTTTCAGATAGGCTTAACAAATGGAGCTTTCTGTATA 1899
                                                                                                                                                                                                                                                                                                    1900 TAAATGTGGAGATTAGAGTTAATCTCCCCAATCACATAATTTGTTTTGTGTGAAAAAGGA 1959
                 274 TATCCATTTTTTTTACTGTTATTTAATTGAAACCATAGACTAAGAATAAGAAGCATCATA 215
                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1909436"
/clone_lib="NCI_CGAP_Lu5"
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/lab_host="DH10B"
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1. .406
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Another Torgan: pooled, Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239,
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Extaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoștomi.
Extaryota; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 508)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Email: cgapbs r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
High quality sequence stop: 464.

Location/Qualifiers
1.508
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                                                                                     3745 GTAAATCCTCAGTTCTTCACCTTTGCACTGTCTGCCACTTAGTTTGGTTATATAGTCATT 3804
                                                                                                                                                                                                   3805 AACTIGAAITIGGICIGIAIAGICIAGACITIAAAITIAAAGITITCIACAAGGGGAGAA 3864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 GTTCAATCTAGTTGTTAGCCAAGGACTCAAGGACTGAATTGTTTTAACATAAGGCTTTTC 167
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                                                                                                                                           347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47
                                                                                                                   106 AAGACTITITITICITCCTCCTCTCCATGAGTTGTGAAATTITAATGCACAACGCTGATGTGGCT
                                                                                                                                                                                                                                                                                                                3925 GTTCAATCTAGTTGTTAGCCAAGGACTCAAGGACTGAATTGTTTTAACATAAGGCTTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3985 CTGTTCTGGGAGCCGCACTTCATTAAAATTCTTCTAAAACTTGTATGTTTAGAGTTAAGC
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IMAGE:2979566 3', mRNA sequence.
AW665401
AW665401. GI:7457948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:2979566"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               508 bp
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Unpublished (1997)
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
infoetmage.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE222433 409 bp mRNA linear EST 03-JUL-2000 hv90g11.xl NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3180740 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 409) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. " 89 c 68 g 176 t
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                                                                                                                                                                                                                                                                                                                                                                                GGTTTACATTACAAGATTCTCACAACAACCCATTGTAGAGGTGAGTAAGGCATGTTACT 3231
                                                                                                                                      2752 AGTCACTTTACTAAAAGATCTTTGTTAACTCAGTATTTTAAACATCTGTCAGCTTATGTA 2811
                                                                                                                                                                                                                                                                                                                       AATTAFAAAATATTGGCAAGAAAAGAAGAATAGTTGTTTAAATATTTTTAAAAAACAC 3111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             149
                                                                                                                                                                  508 AGTCACTTTACTAAAAGATCTTTGTTAACTCCAGTATTTTAAACATCTGTCAGCTTATGTA 449
                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2872 AGATTCTCATATCATCTTGTATCTTAAAGTTTTCATGTGAGTTTTTACCGTTAGGATGATT
                                                                           Length 508
                                                                                                         Indels
                                                                                                        2;
                                                                           DB 10;
                                                                                          Pred. No. 0;
0; Mismatches
                                                                           Score 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE222433.1 GI:8909751
                                                                          Query Match 7.8%;
Best Local Similarity 99.6%;
Matches 506; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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                            175
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ORGANISM
                              BASE COUNT
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AUTHORS
TITLE
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                                            ORIGIN
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="inAcE:180740"
/clone=lib="NoT_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH108"
/note="Corgan: lung; Vector: pT/T3D-Pac (Pharmacia) with a modified poly1inker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "
55 a 72 c 66 g 116 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3803 TTAACTTGAATTTGGTCTGTATAGTCTAGACTTTAAATTTAAAGTTTTCTACAAGGGGAG 3862
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCTGTTCTGGGAGCCGCACTTCATTAAAATTCTTCTAAAACTTGTATGTTTAGAGTTAA 4042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169 TCCTGTTCTGGGAGCCGCACTTCATTAAAATTCTTCTAAAAACTTGTATGTTTAGAGTTAA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.7%; Score 405; DB 10; Length 409;
100.0%; Pred. No. 0;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             413 b
tx47e09.x1 NCI_CGAP_Lu24 Homo
Seq primer: -40UP from Gibco
Location/Qualifiers
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405; Conservative
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AI681542
AI681542.1 GI:
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FEATURES

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DNA Sequencing by: Intellimination information can be found through through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov e column: 06

High quality sequence stop: 565.

Location/Qualifiers

1. 707

Location/Qualifiers

2. 707

Location/Qualifiers

1. 708

Location/Qualifiers

1. 707

Location/Qualifiers

1. 707

Location/Qualifiers

2. 707

Location/Qualifiers

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 707)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2336 TTTTATAGGGGCCTTTTCACTTTCTACTTTTCATTTGTTCTGTTCGAATTTTTATA 2395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2276 AACTGTTAAATGTGGTTTCTCTTCGGGGAGGGGGGGATTGGGGGAGGGGCCCCCAGAGGGG 2335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 TGTCAAAGATATGTTAAGTGTAAAATGCAAGTGGCAAAACACTATGTATAGTCTGAGCCA 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 GATCAAAGTATGTATGTTTTAATATGCATAGAACAAAAAGATTTGGAAAGATATACACCA 288
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                                                                                                 NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tyssue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anote—"Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker: Plasmid DNA from the normalized library NCI_CGAP_Lub was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 rolones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento
                                                         CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 489 Std Error: 0.00
Seq primer: -400P from Gibco.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3863 AAAAGTGTTAAAATTTTTAAAATATGTTTTCCAGGACACTTCACTTCCAAGTCAGGTAGG 3922
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael Emmert: Buck, M.D., Ph.D.
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76 c 67 g 116 t
                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="INAGE:2272744"
/clone="Lih="NCL_CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match
7.6%; Score 398; DB
Local Similarity 100.0%; Pred. No. 0;
Nes 398; Conservative 0; Mismatches
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BI823020
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